| MS9747 D discoldeu AR007403 Sequence AR02596 Paral Lcht AX033167 Sequence AX033159 Sequence | 155769 Sequence 5 M14473 Rabbit musc AX173377 Sequence AX140801 Sequence 193480 Sequence 78 | 191107 Sequence 78 S76509 D158 (A) Ih L20950 D158 (A) Ih AR007408 Sequence U92173 Mus musculu AX207310 Sequence | AR014621 Sequence BD010413 Chimeric 126754 Sequence 54 AF094358 Box fauru | AF050514 Human end N28495 Trypanosoma AJ30784 Hus muscu AX32664 Sequence AX326673 Sequence | S52191 CD11b-leuko AF025985 Paralicht AJ305430 Homo sapi | AR05285 Sequence L31186 Human STS U AX32860 Sequence AX059602 Sequence AX059603 Peralicht | A20465 oliqonucleo H32417 Rat/polyoma AX240922 Sequence S22771 Immunoglobu AX015186 Sequence | AL033823 H.septens M19461 Chicken c-m U7278 Oryclolagus AF174523 Bufo dana U32238 kuman pare B AR17024 Sequence | | linear INV 27-APR-1993 tial cds. DNA. | nning and expression of a 1119 (1991) ideum* |
|--|--|---|--|--|--|---|--|--|--|--|---|
| 55 100 6 25 70 11 20 11 | 5 99 6 83 4 8 91 6 91 6 91 6 91 6 91 6 91 6 91 6 91 | 55 71 6 71 98 3 100 5 51 10 56 66 | 5 5 9 9 7 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | 2000 22 22 22 2001 24 24 | 5 954 9 7 955 5 7 89 5 5 | 55 88 11 55 88 11 55 98 6 57 99 6 | 55555 988 988 988 | 55 55 55 55 55 55 55 55 55 55 55 55 55 | | DDIDDKD 87 bp DNA linear INV 27-APR- NR Ddiscoldeum protein kinase 4 gene, partial cds. NS747 1 G1:167723 Protein kinase 4 gene, partial cds. H59747.1 G1:167723 Protein kinase and ascoldeum (strain Ax.3) DNA. Brickystellum discoldeum (strain Ax.3) DNA. Eukaryolte. Nycetozoa (bum Eukaryolte. Nycetozoa (bum Eukaryolte. Nycetozoa (bum Eukaryolte. Nycetoz | e_alum discoldeum = Molecular Cloning a cioding a developmentally regulated pro- tl. Acad. Sci. U.S.A. 88, 1115-1119 (Location/Qualifiers Doganism="Dictyostellum discoldeum" / Strain="Ax-3" / Strain="Ax-3" / Strain="Ax-3" / Strain="Ax-3" / Strain="Ax-3" |
| 29.6 25.2 25.2 25.2 | 6 25.2 7 25 8 24.8 9 24.6 10 24.6 | 0 111 224 6 0 0 0 112 224 6 0 0 0 0 113 224 6 0 0 0 0 113 224 6 0 0 0 0 0 114 224 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 24 24 25 25 | 22223 2323 233 233 233 233 233 233 233 | 23.8 23.8 6.8 | 222223 222223 266666 | 35 23.4 36 23.4 37 23.4 39 23.4 | . + 2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2. | | RESULT 1 DDIONED LOCUS DEFINITION D. GISCOL ACCESSION M65747.1 KRYMORDS PICCESTON KRYMORDS PICCESTON CRANISH DICCUSES CRCANISH DICCUSES ACTHCRE 1 (DASE AUTHCRE 1 (DASE AUTHCRE 1 (DASE AUTHCRE 1 (DASE AUTHCRE 1 (DASE | JOURNAL PICO. NA MEDLINE 91142122 PEATURES SOUICE |
| • | OM nucleic - nucleic search, using sw model Run on: May 29, 2002, 09:42:16 ; Search time 5865:16 Seconds (without alignments) 17864-019 Million cell updates/sec | Title: | Searched: 1797656 segs, 10463268293 residues Total number of hits satisfying chosen parameters: 843946 | | Maximum Match 100% Listing first 45 summaries | | 5: 90-00; 6: 90-ph:* 7: 90-ph:* 9: 90-pr:* | | 16: em_fun: * 17: em_hum: * 18: em_hum: * 19: em_mu: * | 21: em_on: . 22: em_ov: . 23: em_ph: . 24: em_ph: . 25: em_ph: . 25: em_ph: . 25: em_lp: . 26: em_lv: . 27: em_lv: . 30: em_lv: . 31: em_lv: . 32: em_lv: . 33: em_lv: . 33: em_lv: . | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUNNARIES Result Ouery No. Score Match Length DB ID Description |

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BCT 21-SEP-2000
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Gallusser.A. Karl.J., Lill.H., Stahl.P., Krueger.X. and Borgya,A. Method of identifying n-terminal probnp
Patent: WO 0045176-A 03-AUG-2000;
GALLUSSER ANDREAS (DE): KARL JOHANN (DE): LILL HELMUT (DE):
STAHL PETER (DE): RRUEGER RERSTIN (DE): BORGYA ANNELIESE (DE);
ROCHE DIAGNOSTICS GRAHH (DE)
Location/Qualifiers
                                                                           2 (bases 1 to 96)
Quattro.J.M. and Jones,W.J.
Quattro.J.M. and Jones,W.J.
Direct Submission
Submitted (22-SP-1997) Biological Sciences, University of South Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA Location/Qualifiers
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Escherichia.
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Actinopterygian Fishes
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0.5%; Score 25.4; DB 5; Length 96;
Local Similarity 64.4%; Pred, No. 2.44+05;
Local Similarity 64.4%; Pulsantches 21; Indels
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Best Local Similarity 62.9%; Pred, No. 2.7e+05;
Matches 39; Conservative 0; Mismatches 23; Indels
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/organism-'Paralichthys dentatus'
/db_xref-'taxon:66718'
1. .96
/gene-'LDHA'
/note-'lactate dehydrogenase gene'
/allefe-'PdLDHA2'
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/db_xref="taxon:562"
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Matches 38;
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Paralichthys dentatus Lactate dehydrogenase (LDHA) gene, allele
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Butaryota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi:
Actinopterygli: Neopterygli: Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha: Acanthopterygli: Percomorpha: Pleuronectiformes;
Pleuronectoidel; Paralichthyldae; Paralichthys.
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Havelund.S., Halstr.o slashed.m.J., Jonassen.I., Andersen.A.Sloth.and Markussen.J.
Acylated insulin
Patent: US $750497-A 4 12-MAY-1998;
Location/Qualifiers
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                     /product-"protein kinase 4"
/protein_id-"AAA3189.1"
/db_xref="G1:167724"
/translation="MLLIDDYGHYLTDFGFARRITENTKSHC"
// ranslation="MLLIDDYGHYLTDFGFARRITENTKSHC"
                                                                                                                                                                                                                                              Ouery Match 0.6%; Score 29.6; DB 3; Length 87; Best Local Similarity 59.5%; Pred. Mo. 1.86+04. Mo. Matches 50; Conservative 0; Mismatches 34; Indels
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Pred. No. 1.7e+05;
0; Mismatches 40; Indels
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AR007403.1 GI:3966887
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Quattro, J.M. and Jones, W.J.
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   /codon_start-1
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Best Local Similarity 55.6%;
Matches 50; Conservative 0
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AF025984
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AR007403/c
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Gaps

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18 of 22

Rabit (New Zealand) DNA, clone lambda-charon 4APFK.

Rabit (New Zealand) DNA, clone lambda-charon 4APFK.

Rabit (New Zealand) DNA, clone lambda-charon 4APFK.

Received the season of Chordata. Crantata: Vertebrata: Euteleostomi.

Rammalla: Putheria: Lagomorpha: Leporidae; Oryctolagus.

1 (Nases 1 to 83).

1 (Nases 1
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Rabbit msc.e phosphofructokinase gene, exon 18.
H1473-102702 CI-165622
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/db_xref="taxon:32636"
/note="Reverse primer for RSV A G gene insert"
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/db_xref-"taxon:9986"
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AX173377
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/note=*PFK intron R*
13 c 27 g
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                                                                                          M14473.1 GT:165622
phosphofructokinase.
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                   linear PAT 21-SEP-2000
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(Dases 1 to 70)

(allusser. A. Karl, J., Lill, H., Stahl, P., Kruuger.K. and Borgya.A. Gallusser. A. Warl, J., Lill, H., Stahl, P., Kruuger.K. and Borgya.A. Petent: wo 0045176-73 03-402-2000;

(ALLUSSER ANDELS (DE): KRUEGER KERSTIN (DE): LILL HELHUT (DE): STAHL PETER (DE): KRUEGER KERSTIN (DE): BORGYA ANMELIESE (DE): ROCHE DIAGNOSTICG GYMH (DE)

LOCALION/QUALITIESE
                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision: Enterobacteriaceae;
Escherichia
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0.5%: Score 25.2; DB 6: Length 99;
Best Local Similarity 54.3%; Pred. No. 2.8e+05;
Matches 51; Conservative 0; Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERENCE 1 (bases 1 to 99)
UTHORS Meagher, R.B. and Summers, A.O.
ITLE Metal resistance sequences and transgenic plants
OURNAL Patent: US 5668394 A 5 16.5EP-1997;
TURES Location/Qualifiers
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Sequence 5 from patent US 5668294.
165769.1 GL:2462339
                   ¥NC.
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/db_xref="taxon:562"
19 c 21 g 20 t
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      70 bp
Sequence 3 from Patent WO0345176.
AX033159
AX033159.1 GT:10280023
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21 c 25 g
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Escherichia coli
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DISB (A) [hypervariable minisatellite MS32} [human, individual
MACH, Genomic, 73 nt].
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Enkaryota; Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;
Enkaryota; Metazoa: Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 73)
Monckton.D.C and Jeffrays, A.J.
Monckton.D.C and Jeffrays, A.J.
Minisatellite 'isoallele' discrimination in pseudohomozygotes by
single molecule PCR and variant repeat mapping
Genomics 11 (2), 465-467 (1991)
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GenBank staff at the National Library of Medicine created this
entry | NCB1 gibbsq 76509| from the original journal article.
This sequence comes from Figure 2.
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                                                                              1 (bases 1 to 71)
Toothman, P.J., Ringquist.S. and Gold, L.
High affinity TGF. beta. nucleic acid ligands and inhibitors
Patent: US 5734044-A 78 24-MAR-1998;
Location/Qualifiers
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    .73
    /organism="Homo sapiens"
/db_xref="taxon:9606"
    .73

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   GI:3939577
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$76509.1 GI:243382
                                                                  Unclassified.
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Matches 40; Conserv
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1 (2014)
Cold, L., Janjic, N. and Pagratis, N.
Gold, L., Janjic, N. and Pagratis, N.
High affinity oligonucleotide ligands to growth factors
Patent: US 6207816-A 78 27-MR-2001;
Location/Qualifiers
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Best Local Similarity 63.3%; Pred. No. 3.5e+05; Matches 38; Conservative 0; Mismatches 22; Indels
                                                                                                                                                               linear
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Toothman, P.J., Ringquist, S. and Gold, L.
High affinity TCF. beta. nucleic acid ligands
Patent: US 573144-A 78 24-MAR-1998;
Location/Qualifiers
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Sequence 78 from patent US 5731144.
193480
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AR140801
AR140801.1 GI:14483297
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Sequence 78 from patent US 5731424.
195107
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16 c 22 g
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SOURCE

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RESULT 11 195107/c

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U92173 51 bp mRNA linear ROD 19-FEB-1998 Mus musculus clone IC3 T cell receptor beta chain mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                     House mouse.

Hus musculus.

Eukarotus.

Eukarotus.

Hammalis.

Hammalis.

Hosaes 1 to 51)

Johnston.S.L. and Mettsteln.P.J.

T cell ruceptor diversity in CTLs specific for the CTT-1 and CTT-2 minor histocompatibility antigens

97. Humunol. 159 (6). 2606-2615 (1997)
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Johnston, S. L. and Wettstein, P. J.
Directo, S. L. and Wettstein, P. J.
Direct Submission
Submitted (16-MAR-1997) Immunology, Mayo Clinic, 200 1st St S.W.,
Rochester, MN 55905, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-minor CTT-1 antigen specific CDR3 region*
/codon_statt=1
/product-T cell receptor beta chain*
/proteid_id-*Acca878.1*
/db_xre="G1:2894947"
/translation="VCTCSDPDRYSGNILYF"
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/strain-c578H/6*
/strain-c578H/6*
/clone-*1C*
/cell_type-*cytotoxic T lymphocyte*
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bb 41 GTATTCCAGATACCTGTCAGATCACTACAGTTCACT
               37 CAATTGGAAACTACTGTGGTTAGACGCAG 8
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Location/Qualifiers
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Job time: 11566 sec
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ON Drosophila melanogaster DNA Sequence, complete insertion sequence. 2015050. 120950. 101:04832. 1000500. 101:04832. 100050phila melanogaster (Individual_isolate 820.3) DNA. Drosophila melanogaster (Individual_isolate 820.3) DNA. 15M Drosophila melanogaster (Individual_isolate 820.3) DNA. Prosophila melanogaster (Individual_isolate 820.3) DNA. 15M Drosophila melanogaster (Individual_isolate 820.3) DNA. 100050phila melanogaster Budopterygota: Diptera: Brachycera: Presyota: Neoptera: Endopterygota: Diptera: Brachycera: Prosophila Diptera: I (bases 1 to 89 Drosophila Diptera: Endopterygota: Drosophila. 100050phila. 100050ph
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NEGRECE 1 (bases 1 to 100)

AUTHORS Raveland.S. Halstr.o slashed.m.J., Jonessen.I., Andersen.A.Sioth.

AUTHOR Raveland.S. Halstr.o slashed.m.J., Jonessen.I., Andersen.A.Sioth.

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JOURNAL Patent: US 575049-7 9 12-MAY-1998;

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2 (bases 1 to 98)
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4 and Engels, W.R.
P-eleasent-induced interallelic gene conversion of insertions and deletions in Drosophila melanogaster
Well cell. Biol. 13, 7006-7018 (1993)
94019372
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O.51: Score 24.4; DB 3: Length 98,
Best Local Similarity 56.18; Preci No. 4.5e+05;
Matches 46; Conservative 0; Mismatchics 36; Indels 0; Gaps
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0.55; Score 24.4; DB 6; Length 100;
Best Local Similarity 54.48; Pred. No. 4.5e+05.
Matches 49; Conservative 0; Missatches 41; Indels 3; Gaps
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Squence 9 from patent US 5750497.
AR007408
AR007408.1 GI:1966892
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0: Gaps

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Scoring table:

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Human Secreted pro-
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     WPI: 1997-065462/06. ·
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                      AAT50934:
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                                                                                                                                                                                                                                                                                 1 ctagaagactccccgatga.....ggtttatttaggaaagctc 4990
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                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                          1736436 segs, 858457221 residues
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Listing first 45 summaries
                                                                                                      OM nucleic - nucleic search, using sw model
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AAC19445
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Gapop 10.0 , Gapext 1.0
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Score Match Length Di
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Maximum OB seq length: 100
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Nucleic acid encoding p53-binding protein - which has homology to mouse Mdm2, for use it cancer research

Result No.

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The two subunits of the derivative are covalently connected via disulphide bonds between Cys residues A7/87 and A20/819. The derivative, which may be present as a zinc ion complex, can be used as a fast action treatment for diabetes.
                                                                                                                                                                                                                                                 21; Indels 0: Gaps
They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human insulin derivative: A-chain; diabetes; Zinc ion complex
Ala21 PCR primer #128; ss.
                                                                                                                                              Query Match 0.5%; Score 26.6; DB 21; Length 92; Best Local Similarity 57.1%; Pred. No. 1.7e+03; Matches 36; Conservative 6; Mismatches 21; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acylated insulin deriv. which may be present as a Zinc ic complex—— is used to treat diabetes and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human insulin derivative Ala21 A-chain PCR primer #128.
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                                                                           Sequence 92 BP; 12 A; 9 C; 15 G; 47 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 30; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ86400 standard; DNA; 100 BP.
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Markussen J;
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AAQ86400/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; sa.
                                                                                                                                                                                                                                                                                                                                                                                                                             1122 gtatgagggtgatgacacagaaggagattaaaggagttggaaagtagtacggatgagag 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining CDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences of the 5' region (AAT50934) and 3' region (AAT50935) were detd. for cDNA clone 1, isolated from a mouse 16-day embryo-cDNA library using tumour suppressor p53 as probe. The 5' and 3' regions (AAT50936-37) of another clone were also detd. These sequences showed no significant homology to any known sequence submitted to several databases. A third clone (see also AAT50933) coded for a p53 binding protein designated Mdmx (AAN10206).
                                                                                                                                                                                                                                                                                                                       Query Match 0.5%; Score 27.2; DB 18; Length 78; Best Local Similarity 58.1%; Pred. No. 1e+03; Matches 43; Conservative 2; Mismatches 29; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted, protein 5' EST, SEQ ID NO: 23520.
                                                                                                                                                                                                                                                 Sequence 78 BP; 33 A; 9 C; 22 G; 10 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards J. Duclert A. Glordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 23520; 71pp + CD-ROM; English.
  Disclosure; Fig 2a; 30pp; English
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This invention describes a novel method to detect N-terminal pro-brain natiouetic portide (BMP) in a sample using two antibodies, that recognize different epitopes of the N-terminal pro-BMP. The method can be used for diagnosing heart insufficiency. The recognizent in the method can pro-BMP is useful as a standard in a method to detect N-terminal pro-BMP is useful as a standard in a method to detect N-terminal pro-BMP is useful as a primer used in the cloning of recombinant. This sequence represents a primer used in the cloning of recombinant terminal pro-BMP in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Obery Match

0.55: Score 25.2; DB 21: Length 70:
Best Local Similarity 62.39; Pred: No. 3.7e-03.
Matches 39; Conservative 0: Mamanchies 23; Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification of N-terminal pro-brain natriuretic peptide (pro-BNP) using two antibodies that recognize different epitopes of the N-terminal pro-BNP, useful for diagnosis of hear; insufficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene signature: messenyer RNA: mRNA: relative abundance; frequency; human: cfoning; mapping: non-blased library; diagnosis: detection: cell typing; abunormal cell function; ss.
                                                                                      Brain natriuretic peptide: BNP; primer; human; detection; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Karl J, Lill H, Stahl P, Krueger K, Borgya A, Gallusser A:
                                           Human brain natriuretic peptide N-terminal primer Pro2hum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT22086 Standard; cDNA to mRNA; 89 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1: Page 32: 35pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene signature HUMGS03631.
                                                                                                                                                                                                                                                                                                                                                                                          (HOFF ) ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                                                                                                                   27-JAN-2000; 2000WO-EP00602.
                                                                                                                                                                                                                                                                                                                            99DE-1003489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-1996 (first entry)
     11-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-499359/44.
                                                                                                                                                                                               MO200045176-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy 1838 tg 1839
                                                                                                                                                                                                                                                                                                                         29-JAN-1999;
12-MAR-1999;
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W05514772 - A1
                                                                                                                                                                                                                                        03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 19 69
                                                                                                                 Heart; SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT22086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel use for sequence variants of the human G-protein betal subunit to predict physiological and pathological pathways in the human body. The invention may be used to detect. detect predisposition for, give a prognosis of, or treat a variety of diseases including high blood pressure, hypertonia, cardiac infarction. coronary diseases, immunological diseases, sathma, psoriasis, Crohn's disease, colitis ulectoosa, transplant rejection, mit yor supertitis as or C. This sequence represents a fragment of the human G-protein Gbetal subunit introm 9 which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                      Human: G-protein subunit Gbeta): variant; high blood prossure; asthma; hypertonia; cardiac Infarction; coronary disease; heart disease; circulation disease; diabetes; psychiatric disease; Crohn's disease; tramplodatant rejection; das portasis; colitis ulcerosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of sequence variants of the betal subunit of human G protein to predict, detect, and determine drug targets for diseases including heart, immunological and psychiatric diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507 ctcagtctcaaagaaaaagacagggagcaaagagacaagaaaaatacgtctgg 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 25.2; DB 22; Length 60;
66.7%; Pred. No. 3.4e+03;
ative 0: Mismatches 18; Indels
                                                                                                                                                                                                                                                                                   Human G-protein subunit Obeta3 intron 9 DNA fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60 BP: 6 A; 11 C: 6 G: 37 T: 0 other;
Disclosure; Page 3; 14pp; German.
                                                                                                    RESULT 4
AAR46689/c
ID AAR48689 standard: DNA; 60 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA71594
ID AAA71594 standard; DNA; 70 BP.
XX
XX
AC AAA71594;
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21-FEB-2000; 2000DE-1007587
                                                                                                                                                                                                                                     19-OCT-2001 (first entry)
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Matches 36: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-490007/54.
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Query Match

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5 RESULT

DE10030945-A1. Homo saptens.

AAH48689;

09-AUG-2001.

95US-0427C97

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Metal resistance sequences for producing transgenic plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ28594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA228594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 'SG sequences of given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA. CDNA on mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3' directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-or and from various human tissues; synthesis of CDNA was initiated from the 3'-or and from various human tissues; synthesis of CDNA was initiated from the 3'-or and from the judge to a particular mRNA species. allost CG all the 3'-oriented CDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                               Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abnormance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 25.2; DB 16; Length 89; 62.9%; Pred. No. 4.4e+03; rative 0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metal ion resistance; mercuric ion reductase; merA; mercury; toxtc heavy metal; transgenic plant; mutagenic; bacterial; transposon; T021; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mercuric ion reductase merA PCR mutagenesis primer 307-339S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 89 BP; 39 A; 8 C; 15 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1039; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT92244 standard; DNA; 99 BP
                                               94WO-JP01916
                                                                                            93JP-0355504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 0.5%
Best Local Similarity 62.9%
Matches 39; Conservative
                                                                                                                                                                                                                   Matsubara K, Okubo K;
                                                                                                                                        (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                             WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transposon Tn21
                                            11-NOV-1994;
                                                                                            12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4545 gt 4546
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01-JUN-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT92244;
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IX AAT92244
IX AAT92244
IX AAT97244
IX AAT972
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Organometal: resistance; transcription; translation; regulation; merA; transposon; Tn21; merB; mercuric ion reductase; organometcury lysee; as; transgenic plant; detoxification; metal compound; soil; sediment; primer; aquatic environment; borcemediation; contemination; PCR; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a PCR mutagenesis primer used to mutagenise the mera coding sequence derived from transposon Tn21, to adapt it for plant expressibility. The nucletc acid molecule produced is useful for producing transgenic plants that are resistant to toxic heavy metals (especially mercury) and so can be used remediate and/or revegetate contaminated areas. The bacterial mera gene is derived from the transposon Tn21, which was originally isolated from the Incompatibility Group IncFII resistance plasmid NR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3026 atgtcctgactaaatgtgagagtggtagaggtacaagacccaggtgggcgactcaaggat 3085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 aagacccagctataggtgaagctgttactgctgcattcgcatggaaggcattgaagtgc 61
                                                                                                                                                                                                                                                                                                    DNA encoding mercuric ion reductase in plant-expressible form - for producing transgenic plants resistant to toxic heavy metals
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0.51; Score 25.2; DB 18; Length 99:
Best Local Similarity 54.34; Pred No. 47.7e103;
Matches 51; Conservative O: Mismatches 43; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3086 ttgattttctacaagcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 gigagealacteaageaagecaagtigectatat 95
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Column 43-44; 52pp; English.
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                                                                              (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UYCE-) UNIV GEORGIA RES FOUND INC.
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95US-0427097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ28594 standard; DNA; 99
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                                                                                                                                                        Meagher RB. Summers AO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rugh CL, Meagher RB,
                                                                                                                                                                                                                          WPI; 1997-470112/43
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    21-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1995;
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Gaps

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WPI: 2001-483447/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
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                                                                                                  The invention relates to a nucleic acid molecule comprising a coding sequence for an organometal resistance protein, which is operably concerned for an organometal resistance protein, which is operably linked downstream of and under the regulatory control of a plant expressible transcription and translation regulatory sequence. The organometal resistance legen is sepecially the merk gene from the transposon 710 or the cool merb gene in an expectation of reductates and mercuit of the cross poson 710 or the cool merb gene and mercuit in reducers are useful for producing transgency plants which are capable of efficiently processing mercury. These plants are able to remove or conficient and advance environments providing an efficient coll, sedument, and advance environments providing an efficient this sequence represents a PCR primer used to amplify the 7n2 merk protein wheth is mutated by random mutagenesis (see AA22884 22889 for mutated sequences) and the mutated sequences are expressed in the transgenic plants of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a primer used to generate a synthetic gfp gene by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3026 atgtcctgactaaatgtgagagtggtagaggtacaagacccaggtgggcgactcaaggat 3085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining translational efficiency of codons in cells, comprising introducing synthetic constructs with reporter eness lused in frame tandem repeats of the codon, and measuring expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green fluorescent protein; GFP; reporter gene; codon utilisation; translational efficiency; protein abundance; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ousery Match

Dest Local Statistity 54.39; Preci No. 47.5403; Astrobe Statistity 54.39; Preci No. 47.5403; Astrobe Statistics Statis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0y 3086 tigattitciacaagcaaitgaaccigcettat 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Column 17-18; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA73946 standard; DNA; 54 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-499118/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200042215-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUL-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESOLT 9

AAA73346/C

AAA7346/C

AAAA7346/C

AAAA746/C

AAAAA746/C

AAAAAA746/C

AAAAAA746/C

AAAAAAAAAAAAAAAAAAAAAAA
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CC don followed by a stretch of five identical codons was tisted in frame codon followed by a stretch of five identical codons was tisted in frame immediately upstroam of a 9fp coding sequence to form the synthetic gene. The amplified fragment was cloned into the marmalian expression we coror problem. The amplified fragment was cloned into the marmalian expression we coror problem. Which contains 8440 ori and the CMV promoter, and was used in each of for determining the translational efficiency of a codon in a cell. The synthetic construct was introduced into COS-1 cells and expression of the reporter porter (original procession of the fip reporter constructs was made in which the gip gene is preceded in frame by a tainfam repair of 54 dip reporter constructs was made in which the gip gene is preceded in frame by a tainfam repair to the report of the firstency than their corresponding synonymous codons can be identified. These codons may then be used to replace the less to refer the codons of a polyhucleotide so that there is higher protein expression within undifferentiated optithelial cells such as COS-1 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human: foetal liver; yene expression; single exon nucleic acid probe: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe for measuring human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fecal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ 10 NO 17996; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 05%; Score 25; DB 21; Length 54; Best Local Similarity 69.4%; Pred. No. 3.64-03; Matches 34; Conservative 6; Hismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human foetal liver single exon nucleic acid probe #17996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 54 BP: 9 A: 14 C: 20 G: 11 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG, Hanzel DK, Chen W, Rank DR:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA69691/C
ID ABA69691 standard; DNA; 91 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000: 2000Us-018013.2
26-MAY-2000: 2000Us-0201456
30-JUN-2000: 2000Us-0208465
21-SEP-2000: 2000US-0214667
27-SEP-2000: 2000US-0214667
04-0CT-2000: 2000GS-0214687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived from manks encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNas or polyar RNas derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dy primed cobal libraries. Such ESTs are not well suited for isolating cDNA sequences cDNA sequences have been obtained, the full 5' UTR is rarely included 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs adenomes denome obtained, and genomic ONNAs. SETS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; sa.
                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_ptt_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                              Gaps
                                                                                                                                                                ;
                                                                                                                          Length 91;
                                                                                                                        Ouery Match 0.5%; Score 25; DB 22; Length 91,
Best Local Similarity 61.5%; Proci No. 5.1e+03; Indels
Marches 40; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein 5' EST, SEQ ID NO: 16467.
                                                                    Sequence 91 BP; 28 A; 19 C; 13 G; 31 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 16467; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J, Duclert A, Glordano
                                                                                                                                                                                                                                                                                                                                                                                               AAC12392 standard; cDNA; 77 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0122487
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                                                                                                                                                                                                                                                                      3875 agctc 3879
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                                                                                                                                                                                                                                                                                                          7 ATCTC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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AAC12392/c
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Sequence 77 BP; 27 A; 14 C; 15 G; 21 T; 0 other;

expression and secretion vectors.

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The present sequence for reverse PCR primer for respiratory syncytial vire present sequence for reverse PCR primer for virus (FSV) A G gene insert is used with the forward PCR primer virus (FSV) A G gene insert is used with the forward PCR primer for Aso06999 in the construction of bowine/humaply3-year by primer for the sequence is described in an invention relating to move infectious changed protein (N), and invention relating to move infectious completes a major nucleocapsid protein (N), and a partial or complete PTV vector background polywersse protein (N), and a partial or complete PTV vector background penome. The changed protein (N) and a partial or complete PTV vector background genome combined with one or more heterologous gene(s) or genome combined with one or more heterologous gene(s) or genome complete PTV vector background penome. The chimeric PTV is useful in an attenuated vaccine to elicit an immune response against HPTV3 mad also elicit a polyspecific immune response against HPTV3 and the second chimeric PTV elicits an immune response against HPTV3 and the second chimeric PTV elicit an immune response against HPTV3 and the second chimeric PTV elicit an immune response against HPTV3 and the second chimeric PTV and PTVV3, and where both the first and immune response against HPTV3 and HPTV2 are useful as vaccines to prevent measles and upper or lower respiratory tract infections
                                                                                          ö
                                                                                                                                                              301 gactongtgggtggatctttgccaaaaaatcaattccagatgtggatctcaataagcct 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infectious chimeric parainfluenza virus; antigenic determinant; nucleocapsid phosphoprotein; large polymerase; attenuated vaccine; human PIVJ; HPIVJ; HFIVJ; HFIVJ; RSV; pathogen; measles; PCR pitner; respiratory syncytial virus; respiratory tract infection; bovine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated infectious chimeric parainfluenza virus (PIV), useful in an attenuated vaccine to elicits an immune response against one or more virus(es) sclected from human PIV! (HPIVI), HPIV2 and HPIVI -
                                                                                 0: Gaps
                                                                                                                                                                                                  14 GACTGTGTAGGTGCATTTGTTTAAAAAATATAACTCCCCATTGCCTCTGGGATAAAGTCT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murphy BR, Collins PL, Schmidt AC, Durbin AP, Skiadopoulos MH;
Score 24.8; DB 21; Length 77;
Pred. No. 5.2e+03;
0; Mismatches 27; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse PCR primer for RSV A G gene insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Page 150: 305pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12

AASO66300 Standard; DNA: 92 BP.

X
AASO6930:

XX
AASO6930:

XX
I2-SEP-2001 (first entry)

XX
Infectious chimeric parainfluenza
Munan PYU1; HPIV1; HPIV2; HPIV3; HPIV3;

XX
MULAN PRIVA; HPIV1; HPIV2; HPIV3; HPIV3;

XX
HUMAN PYU1; HPIV1; HPIV2; HPIV3;

XX
HUMAN PRIVA; HPIV2; HPIV3; HPIV3;

XX
HUMAN PEDC-1999;

XX
MOZ00142445-A2.

XX
MOZ00142445-A2.

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MOZ00142445-A2.

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MOZ00142445-A2.

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MOZ00142445-A2.

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MOZ0014245-A2.

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MOZO014245-A2.

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MOZO014245-A2.

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MOZO014245-A2.

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MOZO014245-A2.

XX
MOZO014246-A2.

XX
MOZO0142
         0.5%;
         Query Match 0.5%
Best Local Similarity 60.31
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                       361 tacctcag 368
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2 gaaaatataaaaalactaaccaaaagaagtcigaggtaactatggtaatattaaaactcc 61

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Sequence 92 BP; 20 A; 12 C; 26 G; 34 T; 0 other;
particularly in young children.
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ö Query Match 0.5%: Score 24.8; OB 22; Length 92; Best Local Similarity 63.3%; Prod. No. 5.9e-03; Models 0.8 Matches 38; Conservative 0. Mismatches 22; Indels 0. Caps

AAC11499 standard; cDNA; 94 BP.

AAC11499;

06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEO ID NO: 15574.

Numan: 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Homo sapiens.

EP1033401-A2.

21-FEB-2000; 2000EP-0200610.

26-FEB-1999; 99US-0122487.

(GEST) GENSET.

Dumas Milne Edwards J. Duclert A. Giordano J.

WPI; 2000-500381/45.

New nucleic acid that is a 5' expressed sequence taq (5' EST) for obtaining bobks and genomic Dubbs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

Claim 1; SEQ ID 15574; 71pp + CD-RON; English.

The present sequence is one of a large number of 5' ESTs derived from mRNAs concoding secreted proteins. No OR has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyk? RNAs derived from 50 different issues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the RNA because they are often obtained from oligority primed cONA ilbraries. Such ESTs are not well suited for isolating cDNA sequences been obtained, the clui 5' UTR is rarely included 5' ESTs are derived from finds and even in those cases where longer cDNA sequences have been obtained, the clui 5' UTR is rarely included 5' ESTs are derived from finAsAs and genomic DNAs. 5' ESTs are also used to obtain suil length cONAs and genomic DNAs. 5' ESTs are also used in diagnostic, gene therapy and chromosome mapping procedures with a second contains and account of the contains and account of the second con expression and secretion vectors.

Sequence 94 BP; 46 A; 9 C; 14 G; 25 T; 0 other;

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0.5%; Score 24.8; DB 21; Length 94; 59.1%; Fred. No. 6e+03, Live 2; Mismatches 25; Indels 0; Gaps

Ouery Match
Best Local Similarity 59.1%
Natches 39: Conservative

2595 tgtogtgggggggggtgaaggccatggattacctcattcgaacctgcctcctagtc 1654

70 TTTGGTGATTCAAGTTGAGTGCATTACTTTTCCCTTCCTKCCTKCCTTCCTTCCTTKTTK 11

1655 tetace 1660

ô

ô 8 10 CCTTCC 5

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Ouery Match 0.5%: Score 24.8; DB 21; Length 94; Best Local Similarity 54.3%: Pred. Mo. 66+03; Gendlarity 54.3%: Oneervalue 0: Mismatches 42; Indels 0: Gaps
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Oy 1379 gaccatttgtagacaaagcactgaagcagatggggttaagaagttaattttaagacttc 1438

The present sequence is one of a large number of 5' ESTs derived from mixes encoding secreted proteins.

Continued within the present sequence. The 5' ESTs were prepared from total human RhAs or polyy+ Rhas derived from 10 different tissues. ESTs sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNN because they are often obtained from oligo-off primed coNA.

Contained the Sinch ESTs are not vell suited for isolating coNA sequences they are not vell suited for isolating coNA sequences of RNNs and even in those cases where longer of STSTs are derived from RNNs with intact 5' ends and can therefore becaused to optain full length coNAs and genomic DNNs. 5' ESTs are also used to optain full length coNAs and genomic DNNs. 5' ESTs are also used in diagnostic, forensic que therapy and chromosome mapping procedures. They are used to obtain upsteuem regulatory sequences and to design Muman: 5' EST; expressed sequence tag: scareted protein; cDNA isolation; gene therapy; chromosone mapping; ss. New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic. forensic, gene therapy and chromosome mapping procedutes Sequence 94 BP: 35 A: 10 C: 29 G: 16 T: 4 other: Human secreted protein 5' EST, SEQ ID NO: 19616. Dumas Milne Edwards J. Duclert A. Giordano J. Claim 1; SEO ID 19616; 71pp + CD-ROM; English. 1439 acaactaatqqatqqttccttgcaaaqgqca 1470 62 magatttamtetaggammetattamtaggem 93 RESULT 14
AAC15541/c
ID AAC15541 standard: CONA: 94 21-FEB-2000; 2000EP-0200610. 59US-0122487. 06-OCT-2030 (first entry) WP1; 2000-500381/45. (GEST) GENSET. 26-FEB-1999; Homo saptens. EP1033401-A2 06-SEP-2000. AAC15541;

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The present sequence, a transforming growth factor beta-1 (TGF-beta-1) binding ligand, was identified by Systematic Evolution of Ligands by Exponential enrichment (SELEX). Briefly a candidate mixture of nucleic acids was contacted with TGF-beta-1, and nucleic acids having an increased affinity to TGF-beta-1 partitioned from the remainder of the mixture. The partitioned nucleic acids were then amplified to yield a mixture of nucleic acids enriched for sequences with higher affinity and specificity for binding to requences with higher affinity and specificity for binding to epithelial cell proliferation, or in the diagnosis and treatment of TGF-beta-1 mediated pathological conditions, e.g. fibrocic conditions such as fibroids of the kidney, lung and liver and more acute conditions such as dermal scarring and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF using SELEX, used in the diagnosis and treatment of proliferative
                                                                                                                                                            Transforming: growth factor; beta-1; TGF-beta-1; binding ligand; identification; SELEX; anti-mitogenic; inhibition; cell; systematic Evolution of Ligands by Exponential enrichment; epithelial; proliferation; diagnosis; treatment; fibroids; kidney; lung; liver; dermal scarring; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gold L, Janjic N, Pagratis N, Ringquist S, Toothman PJ;
                                                                                                                             Transforming growth factor beta-1 binding ligand D 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 71 BP; 15 A; 16 C; 22 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 123; 209pp; English.
RESULT 15
AAT65208/c
ID AAT65208 standard; DNA; 71 BP.
                                                                                                                                                                                                                                                                                                                                                                                               960S-0618693.
950S-0458423.
950S-0458424.
950S-0465591.
950S-0479725.
950S-0479725.
                                                                                                                                                                                                                                                                                                                                                                    96WO-US08014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NEXS-) NEXSTAR PHARM INC.
                                                                                              10-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-034387/03.
                                                                                                                                                                                                                                                                                                WO9638579-A1.
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02-JUN-1995;
02-JUN-1995;
05-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                  30-MAY-1996;
                                                                                                                                                                                                                                                                                                                                     05-DEC-1996
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders
                                                               AAT65208;
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Query Match 0.5%; Score 24.6; DB 18; Length 71: Best Local Similarity 65.5%; Pred. No. 5.7e+03; Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Search completed: May 29, 2002, 13:05:25 Job time: 9833 sec

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| 0.5 93 10 0.5 78 10 0.5 85 12 0.5 88 9 | | 0.5 85 9 ATG86378 0.5 86 9 AV532477 0.5 79 9 AA149995 0.5 89 12 A2961698 | 0.5 91 10 D19910 0.5 92 12 AF149669 0.5 93 9 AA669624 | 0.5 99 9 | 0.5 99 10 BEGS4677 0.5 99 10 BEGS4677 0.5 64 9 ABKO8720 | 0.5 68 12 AZS74215 0.5 68 19 AA451873 | 0.5 68 9 A1339161 0.5 68 10 C01741 0.5 94 10 B1943038 C.5 97 12 TA333B01P | ALIGNMENTS | | | | | | | Mashurihit Mouse EST Project Mashington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1800 Email: mousecse@artson.wustl.edu | This clone is available royalty-free through LLNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:699.Nl.: 20ml3 rev2 Er from Amersham Hish quality sequence stop: 82. | |
|---|--|---|---|-------------------------------|---|--|---|------------------------------------|--|--|--|-----------|---|-----------------------|---|---|---|
| 18 19 0 20 21 | C 5 5 5 7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | C 28 | | 0 0 0 | | | 0 0 24444 24446 | | RESULT 1 AA990067 LOCUS | ACCESSION | KEYWORDS SOURCE ORGANISM | REFERENCE | AUTHORS | TITLE JOURNAL COMMENT | | · | FEATURES |
| 4.5 Compugen Ltd. | ch time 3518.59 Seconds (withour alignments) 1944,135 Million cell updates/sec | gqtttatttaggaaagcLc 4990 | | residues | ers: 297742 | | | | | | | | cted by chance to have a of the result being printed, score distribution. | : | DeSCription AA990067 ua58f02.r AA99064 aa44c10.r A1567078 w152907.x B1063432 B1063432 | A136006 qq98409,x B132285 kX19408,y AA154655 mq61008,r T98884 yd61010,r1 A1054386 q176603,x | C5310 C5310 Yujı BE57242 60133139 BF101686 60175418 AA67457 m290a3.r AA46634 093811.s R93104 EST00008 S R4034 Yf81005.s1 AV551027 AV51027 |
| GenCore version 4. Copyright (c) 1993 - 2000 G | nucleic search. using sw model May 29, 2002, 09:13:38 ; Scarch | US-09-676-436-3 4990 1 ctagaagacttctccgatga | IDENTITY_NUC Gapop 10.0 , Gapext 1.0 | 13736207 segs, 6748477542 res | of hits satisfying chosen parameter | length: 0 length: 100 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries | EST:* 1: em_estba:* 2: em_esthum:* | 1: em_estin: 4: em_estow: 5: em_estov: 6: em_estop: 7: em_estro: | 8: em_htc:* 9: 9b_est1:* 10: 9b_est2:* | 11: 95_Atc:* 12: 95_9ss:* 13: em_gss_hum:* | | 5 4 - | | 0.6 70 9 0.6 70 9 0.6 71 9 | 83 9 94 10 100 9 91 10 | 0.5 100 10 253310 0.5 81 10 BE5734.2 0.5 82 10 BF101686 0.5 95 9 AA67645.7 0.5 95 10 A67104 0.5 78 10 A6735.4 0.5 78 10 A6735.4 |

0; Gaps

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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates; Catarthini; Hominidae; Homo.

1. (Pases 1 to 71)

8. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

8. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

8. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

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8. NCI-CGAP http://www.ncbi.nlm.gov/ncicgap.

8. NCI-CGAP http://www.ncicgap.

8. NCI-CGAP http://www.nci
Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZhBHw, pregnant uterus NBHPU, and fetal heart NBHHJ9W) were mixed, and setal heart NBHHJ9W) were mixed, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypitodization reaction. The driver was POR-amplified CDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, and 484468-489479."
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Bukaryota: Butherlar Primetes; Catarrhini; Hominidae; Homo.

Halliar, L., Allen, M., Bowles, L., Dubuque, T., Gersel, G., Jost, S.,

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, Y., Machished (1997, Rochlenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, Washi) Herck EST Project 1997

Contact: Wilson R. School of Medicine

Mashington University School of Medicine

Hashington University School of Medicine

144 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314 286 1810
       AA490364

aa44c10.rl Soares_NhHWPu_Sl Homo sapiens cDNA clone IMAGE:823794 5' similar to SW:NIM1_NEUCR P48479 PROTEIN KINASE NIM-1;, mRNA
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/db_xref="taxon:9606"
/db_xref="ImbGE:823794"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
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Eax: 314 286 1810
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Exa: 314 286 1810
This clone is available royalty-free through LLNL: contact the This clone is available royalty-free through LLNL: contact the This clone is available poor quality
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28mil rev2 ET from Amersham
High quality sequence stop: 1.
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11.1.1.1.2.3 Parastrongyloides trichosuri FL pAMPI vi Chiapelli HCGATICE Parastrongyloides trichosuri FL pAMPI vi Chiapelli HCGATICE Parastrongyloides trichosuri CDNA 5', mRNA Sequence. B1312285 G1:15001471
                                                                                                                                                                                                                                                                                                            COMA Library Preparation: M. Bento Soarcs, Ph.D., N. Fatima Bonaldo, Ph.D. Bonaldo, Ph.D. COMA Library Arrayed by: Greg Lennon, Ph.D. COMA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Clone distribution information can be found through the I.M.A.G.E. Consortlum/LLN at: May-billington: NLCCAPP. Clone distribution information can be found through the I.M.A.G.E. Consortlum/LLN at: Insert Length: 1558 Std Error: 0.00
Seq primer: 400P from Gibco
High quality sequence stop: 76.
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Parastrongyloides tr:chosuri.
Parastrongyloides (Lichosuri.
Eukaryota; Metazoa; Namatoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Parastrongyloides.
[ (bases 1 to 54)
McCarter,J., Cilifon.S., Chlapelli,B., Pape,D., Martin.J., Wylie,T.
Dante.M., Marra,M., Hilller,L., Kucaba,T., Thelsing,B., Bowers,Y.
                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
                 Homo Sapiers

Bukaryota: Metazoa: Chordata: Craniata; vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates: Catarhini: Hominidae: Homo.

1 (bases 1 to 8)

Wci/Minos-GGAP http://www.ncbi.nlm.nih.gov/ncicqap.

Mational Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/GROA). Tumor Gene Euther (CGAP/GROA).
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83 bp mRNA linear EST 16-FFB-1999
DEFINITION #99409409 x1 WCI_CGAP_BEn25 Homo Sapiens CDNA clone INAGE:2019185 3',
ACCESSION AI360096
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Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
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Amphibia: Batrachia; Anura: Mesobatrachia: Pipoidea; Pipidae;
Xenopodinae, Xenopus.
I (basea i to 81)
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2 THTTCTGCCACACAGAACAGATGAACTTAATAAATTACAATGCACTGCACTGCTT 51
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/clone_iib-*NIBB Mochil normalized Xenopus tailbud
library*
                      Ouery Match

O.64: Score 28.5: OB 9: Length 71:

Best Local Similarity 64.21: Pred. Mo. 1.78+04.

Matches 4.3: Conservative 0: Mismatches 24: Indels

Matches 4.3: Conservative 0: Mismatches 24: Indels
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Contact: Tadasu Shin-1
Centac For Genetic Resource Information
Mational Institute of Genetics
1111 Wite Mishims, Shizuoka 411-8540, Japan
Fel: 81-559-81-6855
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/dev_stage="stage 25"
15 a 11 c 11 g 42 t
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/db_xref-"taxon:8355"
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Xenopus laevis
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Homo sapiens
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                                                                             Wilson, W. The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway. Box 8501. St. Louis. WO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu)
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu)
University Genome Sequencing Center St. Louis.
Putative full length read
The vector to vector length is 95
Seq primer: -40RP from Globco.
Seq primer: -40RP from Globco.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AALD4055 mg61c08.rl Scares_thymus_2Nbwr mus musculus cDNA clone IMACE:583214 S' similar to SW:RCC4_MOUSE P08414 CALCIUM/CALWODULN-DEPENDENT PROTEIN KINASE TYPE IV CATALYIIC CHAIN ;, mRNA sequence. AA154655
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Leh, Hartfin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
. Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, M., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Walerston, R. and
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91 bp mRNA linear EST 17-MAR-1995 yddiddlo.rl Soares fetal liver spleen lNFLS Homo sepiens cDNA clone IMAGE:112723 5' similar to gb:x56468_rnal 14-3-3 PROTEIN THETA THERA SEQUENCE.
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1 (bases 1 to 91)
1 (bases 1 to 91)
1 (hiller C., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Multman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Riktin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Willlamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                         Washington University School of MedicineP
Washington University School of MedicineP
Washington University School of MedicineP
Half Spress Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 316 286 1810
Final: mousestiwatson.wustl.edu
This clone is available royality free through LLML: contact the
IHAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28MJ rev2 from Amersham
High quality sequence Stop: 1.
Location/Qualifiers
1. .100.
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/sex="male"
Waterston, R.
The Washiv-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
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/dev_stage="4 weeks"
/lab_host="DH108"
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15 Caronimabditis elegans.
16 Caenorhabditis elegans.
17 Caenorhabditis elegans.
18 Mayditude: Peloderinae: Caenorhabditis.
18 Koharair. Motohashi.T. Tabara.H., Watanabe.H., Sugimoto.A., Sano.
18 Koharair. Motohashi.T. Tabara.H., Watanabe.H., Sugimoto.A., Sano.
18 Koharair. Motohashi.T. Tabara.H. Watanabe.H., Sugimoto.A., Sano.
18 Koharair. Motohashi.T. Tabara.H. Watanabe.H., Sugimoto.A., Sano.
18 M. Hiyaka.A. and Nishigari.A.
18 Contact: Yuji Kohara
18 Contact: Yuji Kohara
18 Contact: Yuji Kohara
18 1559-81-684
19 Taxi. 81-559-81-684
10 Taxi. 81-559-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-*Homo sapiens*
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/clone_ilb=*Mc_CGAP_Ov26*
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/ser-*[maile*
/dev_Stage-*adult_
/dev_Stage-*adult
LOCUS
DEFINITION CS3310 YUJ; Kubara unpublished CDNA Caenorhabdilis elegans CDNA
ACCESSION CS3310 YUJ; Kubara unpublished CDNA Caenorhabdilis elegans CDNA
ACCESSION CS3310.1 CI:2391067
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/clone="vk259b3"
/clone="vk259b3"
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/fujs Kohara unpublished cDMN"
/sex="hermanhrodile, male"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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AL Unpublished (1995)
Contact: Wilson My Washty School of Medicine
Mashington University Box 8501, St. Louis, MO 63108
Test: 314 286 1800
Email: estwatuon.wustl.edu
Insert Size: 715
High quality sequence Starts: 1 High quality sequence Stops: 1
High quality sequence Starts: 1 High quality sequence Stops: 1
High quality sequence Stop: 11
For furber information. Trace considered overall poor quality
Insert Length: 715 Std Error: 0.00
Seq primer: Mi3PP
High quality sequence Stop: 1.
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//dev_aloge*20 week-post conception fetus*
//deb_host*20 week-post conception fetus*
//deb_host*20 week-post conception for fetus*
//deb_host*20 with a fetus for fetus 
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q1/6e03.x1 MCI_CGAP_Ov26 Homo sapiens cDNA clone IMAGE:1862428 3',
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Bukaryota: Metazoa: Chordata: Cranlata: Vercebrata: Euteleostomi:

Bukaryota: Metazoa: Chordata: Cranlata: Vercebrata: Euteleostomi:

1 (Bassa 1 to 9)

MCI-GRAP HES-/vvv.ncbl.nlm.nlh.gov/nclcgap:

MCI-GRAP HES-/vvv.ncbl.nlm.nlh.gov/nclcgap:

MCI-GRAP Institute, Cancer Genome Anatomy Project (CCAP),

Tunor Gene Index
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Contact: Robert Strausberg, Ph.D.
Email: cgepbs-remeil.inih.gov
Tissue Procurement: Nonica Brown, M.D., Elisc Kohn, H.D., Michac.
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cch (1.54) Score 27.4; Da 10; Length 91; 11.5imilarity 54.44; Pred. No. 3.9e-04; (1.5coservetive ); Misnatches 36; Indels 0; Gaps
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/Clone="IMAGE:112723"
/Some="IMAGE:112723"
/Some="IMAGE:12723"
/Some="IMAGE:12723"
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A1054386
A1054386.1 GI:3322173
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/db_xref="traxon:10090"
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Mammalla: Eutheria: Rodentia: Sclurognathi; Muridae; Murinae; Mus.
Mammalla: Eutheria: Rodentia: Sclurognathi; Muridae; Murinae; Mus.
Mational institutes of Health, Mammalian Gene Collection (MGC)
NithMGC http://mgc.nci.nih.gov/.
NithMgC http://mgc.nci.nih.gov/.
Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emall: egapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I. M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I. M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 81.
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mBNA sequence.
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/dev_stage="varied"
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Outpublished (1997)
Contact Robert Strausberg, Ph.D.
Contact Robert Strausberg, Ph.D.
Contact Robert Strausberg, Ph.D.
Email: cqapbs:rfmail.nth.90v
Tissue Procurement: Chistopher Moskaluk, M.D., Ph.D., Michael R.
Finster Procurement: Chistopher Moskaluk, M.D., Ph.D., Michael R.
Contact Library Preparation: W. Hento Soares, Ph.D.
CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: KRI-CGMP Clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
Now-bio.lini.gov/bbpt/mage/Lingue hual
Insert Length: 820 Sed Error: 0.00
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High quality sequence stop: 87.
Local England Sequence stop: 87.
Local England Sequence Stop: 87.
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Schistosoma manson!
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Strigetidad schistosomatoidea: Schistosoma.
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Saber: M. Hanied.M. Elforssaki.W.N. Romeih.M. Ahmed.M. Wohareb
Schistosoma mansoni conna.
Urpublished (1995)
Contact: M.A. Saber: M. Hamied. W.N. El Yassaki, M. Romeih, H. Hill Hamied. M. Wohareb
Thines (1995)
Contact: M.A. Saber: M. Hamied. W.N. El Yassaki, M. Romeih, H. Hari Bistochem. Strysomanski.
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/CLONE-"INAGE.1588653*
/CLONE-"INAGE.1588653*
/Lissuc_Lyper"2_pooled tumors (clear cell type)*
/lab_host-"Phil08*
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Imbaba, P.O. 80x 12411, Giza, Egypt.
Pax: 202 3128276
Fax: 202 3121167
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/clone='lph-Soares mouse lymph node NDMLN'
/sat=male,
/tissue_rype-lymph node'
/devisitage-4 weeks
/devisitage-4 weeks
/devisitage-4 weeks
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Namaalia; Eutheria; Rodentia; Sciurognathi; Huridae; Murinae; Nus.
1 (bases 1 to 87)
Harrah, Hillier, Allen, Bowles, M., Dietrich, N., Dubuque, T., Garsah, S., Huther, T., Lacy, M., Le, N., Martin, J., Morris, N., Schelenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Marerston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matticour, Are Mash Wouse EST Project
Onpublished (1996)
Contact: Marra M/Mouse EST Project
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Hashlagton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Email: M-Saber@FRCU.EUN.BG
Seq primer: Sk.
Location/Qualiflers

lucation/Parallers

lucation/Parallers

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lucation/Parallers

lucation/Parallers

lucation/Parallers

lucation="Skibackooma manson!"

/db.xre="texton:6183"

/clone="Skibackooms on Shibackooms on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       701 tcaaagtcgactatgg 716
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                                                                                                                                                                                                                    source
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ORIGIN
                                                                                                                                                        FEATURES
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Search completed: May 29, 2002, 11:17:02 Job time: 7404 sec

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Page 1

| 28 22.2 0.4 71 2 US-08-465-591A-75 Sequence 29 22.2 0.4 71 2 US-08-465-594A-75 Sequence 30 22.2 0.4 71 4 US-08-973-114-260 Sequence 31 22.2 0.4 71 4 DS-08-973-114-260 Sequence 31 22.2 0.4 71 5 PCT-0856-08014-260 Sequence 31 22.2 0.4 71 5 PCT-0856-08014-260 Sequence 31 22.2 0.4 85 2 US-08-488-4628-4638-494 Sequence | 22.2 U.4 65 2 US-UB-480-4018-99 22.2 0.4 85 2 US-UB-480-4999 22.2 0.4 85 E US-UB-4804-552A-99 | 34 22.2 0.4 67 10.500 0474.77 59 Sequence 36 22.2 0.4 87 10.508 110 1266.3 56 514 Sequence 37 21.8 0.4 54 105 05 05 05 05 05 05 05 05 05 05 05 05 0 | 39 21.8 0.4 81 3 4 4 1 21.6 0.4 655 3 4 4 1 21.6 0.4 655 3 4 4 1 21.6 0.4 655 3 4 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | 21.6 0.4 85 2 05-08-602-09-23 Sequence 21.6 0.4 89 1 05-08-602-09-13 Sequence 21.6 0.4 93 1 05-0 | 21.0 0.4 95 5 05-00-473-440-113 Sequence | ALIGNMENTS | RESULT 1 | ence 4, A | RULIN | ADDRESSER: No. 57504970 No. 5750497disk of No. 5750497th America, Inc. STREET: 405 Lexington Avenue, 64th Fluor CITY: New York STATE: New York | COUNTRY: United States of America | COMPUTER EACASHEE FORM: HEDDIUM TYPE: FLOPEY GLISK COMPUTER: IEM PC COmpatible | OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.25 CHURCHY ADDI-CAPTION DATA | APPLICATION NUMBER: US/UB/400, 256 | CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: | : NAME: Lambiris, Elias J. : REGISTRATION NUMBER: 33.728 | REFERENCE/DOCKET NUMBER: 3985.220-US | : TELEPHONE: 212-867-0123 | INFORMATION FOR SECTION 4: | SEQUENCE LARRALIEMISTICS: | TYPE: nucleic acid | TOPCLOCY: linear | : MOLECULE TIPE: UNA US-08-400-256-4 | | Query Match 0.5%; Score 26; OB 1; Length 100; | vative (| Qy 4469 aagaasgaagcclaglagaalatggaacttggaaauttotottaatoectactgtatgtaa 4528 |
|---|---|---|---|--|---|---|--|---|---|--|-----------------------------------|--|--|--|--|--|---|---|--|---------------------------------------|---|--|---|---|---|---------------------------------|---|
| GenCore version 4.5 Copyright (c) 1993 - 2000 Co≡pugen Ltd. | OM nucleic - nucleic search, using sw model | Run on: May 29, 2002, 10:15:51; Search time 94.14 Seconds (without alignments) 13020.089 Million cell updates/sec | Title: US-09-676-436-3 Perfect score: 4990 Sequence: 1 ctagaagacttctccgatgaggtttattttaggaaagctc 4990 | Scoring table: IDEMITTY_MUC Gapon 10.0 , Gapext 1.0 | Searched: 383533 seqs, 122816752 residues | Total number of hits satisfying chosen parameters: 613726 | . Winimum DB seq length: 0 Maximum DB seq length: 100 | Post-processing: Minimum Match OB Maximum Match 100% Listing first 45 summaries | Database : Issued_Parents_NA:* 1. /cqn2_6/ptodata/lina/5A_COMB seq:* 2. /cqn2_6/ptodata/lina/8a_COMB seq:* 3. /cqn2_6/ptodata/lina/AA_COMB seq:* 4. /cqn2_6/ptodata/lina/AA_COMB seq:* 5. /cqn2_6/ptodata/lina/ACOMB seq:* 6. /cqn2_6/ptodata/lina/PCTUS_COMB seq:* 6. /cqn2_6/ptodata/lina/PCTUS_COMB seq:* | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | SUMMRIES | Result Overy No. Score Match Length DB ID Description | 26 0.5 100 1 US-08-400-256-4 Sequence 4. 26 0.5 100 3 US-08-09-36-4 Sequence 4. | 3 25.2 0.5 99 1 US-08-427-097-5 Sequence | 5 24.6 0.5 71 1 US-08-428-423A-78 Sequence 78 6 24.6 0.5 71 1 US-08-458-78 Sequence 78 | 24.6 0.5 71 4 US-08-973-124-78 Sequence 24.6 0.5 71 5 PCT-US96-08014-78 Sequence | 9 24.6 0.5 72 3 US-09-100-664A-5 Sequence | 24.4 0.5 100 3 US-08-975-365-9 Sequence | 24 0.5 97 1 US-08-474-633A-63 Sequence | 24 0.5 83 1 US-08-672-158A-8 Sequence | 23.6 0.5 87 2 US-08-631-751A-4 Sequence 23.4 0.5 77 1 US-07-679-052A-8 Sequence | 23 0.5 60 3 US-08-643-704A-17 Sequence | 22.8 0.5 76 1 US-08-246-583-9 | 21 22.8 0.5 96 3 US-08-484-322-5 Sequence 22 22.6 0.5 77 1 US-07-679-052A-10 Sequence | 22.4 0.4 90 1 US-08-123-702-23 Sequence 21, | 22.4 0.4 97 1 US-08-182-175A-48 | 22.4 0.4 97 1 US-OB-474-633A-57 Sequence 57, 22.4 0.4 97 5 PCT-US92-06412-48 Sequence 48, |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NO. 60110070 NO. 6011007disk of NO. 6011007th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9) AAGTCTGACGACACTAAGGGTATCGTTGAACAATGTTGTACTTCTATCTGTTGTACTTGTAC 38
Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.5%; Score 26; DB 3; Length 100; Best Local Similarity 55.6%; Pred. No. 6.1e+02; Matches 50; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
CTATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NOWBER: US/08/975,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lamblis, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMUNICATION INFORMATION:
TELECHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oy 4529 tatttacataaagactgtgctgagaagcag 4558
                                                          4529 tattlacalaaagactgtgctgagaagcag 4558
                                                                                                                                                                                                                                                                              APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 CAATTGGAAAACTACTGTGCTTAGACGCAG 8
                                                                                                   37 CANTIGGAAACTACTGTGCTTAGACGCAG 8
                                                                                                                                                                                           US-08-975-365-4/c
Sequence 4, Application US/08975365
Patent No. 6011007
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : MOLECULE TYPE: DNA
US-08-975-365-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-427-097-5
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Sequence 5, Application US/38427097 Patent No. 5668294

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0: Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HESULT.

1 US-08-87-5
1 Sequence 5, Application US/08878957
2 Sequence 5, Application US/08878957
3 Sequence 5, Application US/08878957
3 Sequence 5, Application Sequence 5, Application September 10: Applicant Summers, Anne 0.

APPLICANT: Number Color L.

TILLE OF INVENTION: Hetal Resistance Sequences and TILLE OF INVENTION: Transgenic Plants
NUMBER OF SEQUENCES: 34
1 NUMBER OF SEQUENCES: 34
2 NUMBER OF SEQUENCES: 34
3 NUMBER OF SEQUENCES: 34
3 NUMBER OF SEQUENCES: 34
5 COURESPONDENCE ADDRESS:
5 COURTS STATE: Colorado
5 COUNTRY: US
GENERAL INFORMATION:
APPLICANT: Meadier, Richard B.
APPLICANT: Meadier, Richard B.
APPLICANT: Sommers, Anne O.
TITLE OF INVENTION: Metal Resistance Sequences and
TITLE OF INVENTION: Transgenic Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OFREATING SYSTEM: PC -COS/MS-DOS
OGTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/427,097
FLING DATE: 21-ARR-1995
CLASSIFICATION: 800
                                                                                                                                           ADDRESSE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oy 3086 ttgattttctacoagcaattgaacctgcctttat 3119.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc - "Oligonucleotide"
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCHEVAGENT INFORMATION:
NAME: FETEET DOING M
REGISTRATION NUMBER: 33.78
REFERENCE/DOCKET NUMBER: 40.94
TELEPHONE: (303) 499-8080
INFORMATION INFORMATION:
TELEPHONE: (303) 499-8080
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : ANTI-SENSE: NO US-08-427-097-5
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US-08-458-423A-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outry Match

0.5%, Score 25.2; DB 2; Length 99;
Best Local Similarity 54.3%, Pred. Mo. 16-03;
Matches 51; Conservative 0; Mismatches 43; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: ROOPPY disk
MEDIUM TYPE: TOOPPY disk
COMPUTER: INH PC COMPALIDE
OPERATING SYSTEM: PC - VOS/MS-DOS
SOFWARE: PARENTIN RELEASE 11.0, Version #1.30
CURRENT APPLICATION NUTBER: US/08/978,957
FILING DATE: 19-JUN-1997
CLASSIRICATION: BOD
PRIOR APPLICATION NUTBER: US 08/427,097
FILING DATE: 21-APR-1995
ATORNEVAGER INFORMATION:
NAWE: FERDER: DORNG N
RETERENC/DOCKET NUMBER: 40-94A
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
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Squence 78, Application US/08458423A

Squence 78, Application US/08458423A

Patent No. 5731144

GREEAL INFORMATION: J TOOTHANN

APPLICANT: STEVEN RINGOUIST

APPLICANT: STEVEN RINGOUIST

TITLE OF INVENTION: HIGH AFFINITY TGFS NUCLFIC

TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS

CORRESPONDENCES: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIP: 80111
COMPUTER READMBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Swanson and Bratschun, L.L.C. SYREET: 8400 East Prentice Avenue, Suite 1200 STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy 3086 ttgatttctacaagcaattgaacctgccttat 31)9
bb 62 gGAGCATACTCAACCAAGCAAGCAAGTGCGCTATAT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
RPLICATION MINERS: US/08/458,423A
FILING DATE: 2-JUNE-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 99 base pairs TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ANTI-SENSE: NO
US-08-878-957-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NS.
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PRIGR APPLICATION WINERS: 07/14.131

PRICRATION WINERS: 07/24.48

PRICRATION WINERS: 07/25.48

PRICRATICH WINERS: 08/25.48

PRICRATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 0.5%: Score 24.6; DB 1; Length 71; Best Local Similarity 65.5%; Pred. No. 1.2e+03; Matches 36; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 78, Application US/08973124

Sequence 78, Application US/08973124

Patent No. 6207816

CENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
ITILE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
ITILE OF INVENTION: LIGANDS TO GROWTH
ITILE OF INVENTION: EACTORS
NUMBER OF SEQUENCES:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 8011
CCMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IRM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 6.1
CURRENT APPLICATION DATA:
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,524
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER:1993
PRIOR APPLICATION NUMBER: 08/117,991
FILING DATE: 17-AUGUST-1992
ATPOLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
ATPOLICATION NUMBER: 33,960
REFERENCE/FOXCET UNMBER: 33,960
REFERENCE/FOXCET UNMBER: 33,960
RECISTRATION NUMBER: 33,960
RECISTRATION NUMBER: 33,960
RECISTRATION NUMBER: 33,960
RECISTRATION NUMBER: 33,960
RECEPHONE: (303) 793-333
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STAPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA
APPLICATION NUMBER: PCTUS96/08014
FILING DATE: 30-MAY-1996
PRIOR APPLICATION DATA
APPLICATION NUMBER: 084/58,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1955
PRIOR APPLICATION DATA: 08/465,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Innear
HOLECULE TYPE: DNA
US-08-458-4248-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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FILLING DATE: 05-JUNE-1995
FRIGH APPLICATION MATA:
PULICATION MATA:
PULICATION MATA:
FILLING DATE: 07-JUNE-1995
FRIGH APPLICATION MATA:
FRIGHT CANE: 07-JUNE-1995
FRIGH APPLICATION MATA:
FRICHE CANE: 07-JUNE-1995
FRICH CANE: 07-JUNE-1995
FRILING DATE: 07-JUNE-1995
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ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America. Inc. STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oy 3694 attggagaaagccagtatgggaaggtgtacacctgcatcagcgtcgacaccggggagctg 3753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery March

Ouery March

Best Local Similarity 59.2% Perds No. 1.36+03.

Best Cocal Similarity 59.2% Perds No. 1.36+03.

Marches 42: Conservative 0: Mismatches 29; Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTER: New York
COUNTER: United States of America
LIP: 1074-6401
COMBUTER: United States of America
LIP: 1074-6401
COMBUTER: Floppy disk
NEDIOW TYPE: Floppy disk
COMBUTER: Ploppy disk
COMBUTER: Postentin Release 1.0, Version B1.25
SOFTWARE: Patentin Release 1.0, Version B1.25
CURRENT APPLICATION DATA
APPLICATION WHORE: US/08/400,256
FLING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATORNEY/ACENT INFORMATION:
NAME: Lamblris, Elias J.
REGISTRATION WHORE: 33.728
REGISTRATION WHORE: 33.728
RECISTRATION WHORE: 3.729
RECISTRATION WHORE: 3.720
RECISTRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-08-400-256-9/C
Sequence 9, Application US/08400256
Sequence 9, Application US/08400256
Sequence 9, Application US/08400256
GEREAL INFORMATION:
APPLICANT: Havelund, Svend
APPLICANT: Halstoom, John
APPLICANT: Andorsen, ID
APPLICANT: Andorsen, Asser Sloth
APPLICANT: Naforsen, Asser Sloth
TITLE OF INFORTION: ASSER SIOTH
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSED NO 57ACACT
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3754 atggccatgaa 3764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
HOLECULE TYPE: DNA
US-08-400-256-9
                                                                                                                                                                                                                                                                                                          TOPOLOGY: linea NOLECULE TYPE: CD HYPOTHETICAL: NO US-09-100-664A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Ouery Match
6.5%; Pref. No. 12e+03;
Best Local Similarity 65.5%; Pref. No. 12e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oy 3958 gaacatgtgattaggctgtattcaaagcagatcaccattgcgatcaacgtcctcc 4012
bb 56 GAAGACATAGTAATAAAAAARARARACCCCCCTGGCGGTGGTCCTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5. Application US/09100664A
Sequence 5. Application US/09100664A
GENERAL INFORMATION:
APPLICANT: YOUNG, MICHAEL W
APPLICANT: RLOSS, BRIAN
APPLICANT: RLOSS, BRIAN
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
WINNER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALAUBET 6. Jackson
STREET: 411 HACKENSEC AVORDLE, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDUNT TREE FLOPPY GISK
COMPUTER: ISA FC compatible
COMPUTER: ISA FC compatible
COMPUTER: ISA FC compatible
COMPUTER: ParentIn Release #1.0, Version #1.30
CURRENT APPLICATION AND A.

CURRENT APPLICATION MUNER: US/09/100,664A
FILING DATE: 19-UNH-1998
CLASSIFICATION #135
ATTORNEY/AGENT INPORANTION:
NAME: JACKAON ESQ., DAVIG A.

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 2600-1-221
                                                                                                                                                                                                                                                                     PRILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
RPLING DATE: 07-20NE-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PROPREY APPLICATION NUMBER: 08/618,693
FILING DATE: 20-4ARCH-1996
ATTORNEY AGENT INFORMATION:
NAME: BARTY J. SARGON:
REFERENCE/COCKT NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base polis
TYPE: nucleac acid
STRANDEDNESS: single
STRANDEDNESS: single
HOLECULE TYPE: DNA
PCT-US96-08014-78
PRIOR APPLICATION DATA:
APPLICATION WHBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION GATA:
APPLICATION MINBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,735
APPLICATION NUMBER: 08/479,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 Hackensi
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
2.IP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-100-664A-5
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APPLICANT: SAVETION CALL Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
UNIMER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function= "synthetic storage protein
/product= "protein"
/gene= "ssp"
/standard_name= "5.11.11.5"
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 107 Market Street
CITY: Hilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READALE FORM:
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: MICROSOft Word, 4.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 ANGUET 1991
ATTORNEY-AGENT INFORMATION:
NAME: LINGA AXAMETLY FLOYD
REGISTRATION UNBER: 33,692
REFERENCE/DOCKET NUMBER: 38-692
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB-1031
                             RESULT 12
US-08-182-175A-54
; Sequence 54, Application US/08182175A
; Patent No. 555923
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (302) 892-7949
TELEX: 83440
INFORMATION FOR SEO ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH. 97 base palrs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN: E. COLI
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1180 agtgaagaagaa 1191
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-182-175A-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Alonessen, John
APPLICANT: Andersen, Asser Sioth
APPLICANT: Andersen, Asser Sioth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
HUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE No. 60110070 No. 6011007disk of No. 6011007th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                      4469 aagaatgaageetagtagaatatggaettggaaaaitetettaateactaetgtatgtaa 4528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 0.54; Score 24.4; DB 3; Length 100; Best Local Similarity 54.44; Pred. No. 1.7e+03; Matches 49; Conservative 0; Mismatches 41; Indels 0; Gaps
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 AAGTCTGACGACGACGCTAAGGGTATCGTTGAACAATGTTGTACTTGTACTTGTACTTGTAC 38
                                                                                                                                                                                      ö
Query Match 0.5%; Score 24.4; DB 1; Length 100; Best Local Similarity 54.4%; Pred. No. 1.7e+03; Matches 49; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: "New York
COUNTYR: United States of America
ZIP: 10174-6401
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compartible
OPENATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILLING DATE:
RILLING DATE:
FILLING DATE:
FILLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/ACENT INFORMATION:
NAME: Lamblits, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
TELECHMUNICATION INFORMATION:
TELECHMONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oy 4529 tatttacataaagactgtgctgagaagcag 4558
                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-975-365-9/c
; Sequence 9, Application US/08975365
; Patent No. 6011007
; RENERAL INFORMATION:
RAVELUNG, SVEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 100 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     us-08-975-365-9
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                                                                                                        1120 gagtatgagggtgatgacacagaaggagaattaaaggagttggaaagtagtacggatgag 1179
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Query Match 0.5%; Score 24: DB 1; Length 97; Best Local Similarity 58.3%; Pred. No. 2.2e+03; Matches 42; Conservative 0; Mismatches 30; Indels
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RESULT 14
PCT-0592-06412-54
Sequence 54, Application PC/TUS9206412
Sequence 54, Application PC/TUS9206412
GENERAL INFORMATION
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
TITLE OF INVENTION: Sh. Riceler
TITLE OF INVENTION: Sh. Sh. Cheller
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS
ADDRESSEE: E.1. 400 March Chemours and Company
STREET: 1007 March Struct Structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oquery Match

0.5N: Score 24: UB 5; Length 97;

Best Local Similarity 58:3N; Pred No. 2.2e+03;

Macches 42: Conservative 0; Mismetches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                   STATE: Delaware
COUNTRY: USA
ZIP: 19896
COMPUTER RAIJBALE FORM:
MEDIUM TYPE: Floppy 01sk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Mord, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
CLASSIFICATION: 540
PROG PAPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 1991
ATTORNEY/AGENT INFORMATION:
NAME: LAIDGA AXAMETLY FlOYd
REGISTRATION UMBER: 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SED ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTECLE TYPE: DNA (genox
ORICINAL SOURCE:
STRAIN: E: COLI
CELL TYPE: DN5 alpha
IMPDIATE SOURCE:
FLATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LCCATION: 2 .88
COATION: 2 .88
OTHER INFORMATION: //
OTHER INFORMATION: //
PCT-US92-06412-54
                                                                                                                                                                                                                                                                                                                                                Wilmington
Delaware
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery March 0.54; Score 24; DB 1; Length 97; Best Local Similarity 58.34; Pred. NO. 2.2e-03; Marches 42; Conservative 0; Mismatches 30; Indels
                                                                                                               CREERAL THE CONSTICUTED BONT DE NEMOURS AND APPLICANT: COMPANY TITLE OF INVENTION: METHOUS FOR INCREASING TITLE OF INVENTION: INCREASING TITLE OF INVENTION: INCREASING TITLE OF INVENTION: AND THROOMING COMPENTIALLS OF INVENTION: OF THE SEEDS OF PLANTS INUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FUNCH
HEDINH TIPE. ELOPPY DISK
COMPUTER: JBM PC COMPATIBLE
COMPATING STERE: PC.7057/MS-FDS
SOFTWARE: NTCROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
PRILICATION HOUBER: US/08/474,633A
FILLED DATE: NTCROMATION:
MAME: BARBARA C. SIEGELI
REDISTRATION NUMBER: 30,684
REPERPUED/DOCKET NUMBER: 30,684
REPERPUED/DOCKET NUMBER: 30,684
REPERPURE: 030-992-9331
FELECOMUNICATION HUMBER: BB-1037-C
TELECOMUNICATION HUMBER: BB-1037-C
TELECOMUNICATION FOR SEQ 100-992-9331
FELECOMUNICATION FOR SEQ 100-953-9331
FERGIFIES 93 DASSE PRIFES
FINANDENDESS: GOUDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function- *synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          storage protein
/product- protein
/gene. "ssp."
/standard.name-
"5.11.11.5"
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: I. ID PORT DE NEMOURS ADDRESSEE: AND COMPANY STREET: 1007 AARKET STREET
CITT: WILMINGTON
ESULT 13
US-08-414-633A-63
Sequence 63. Application US/08474633A
Settent No. 577861
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
PE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11near
MOLECULE TYPE: DNA (genor
ORIGINAL SOURCE:
STRAIN: E. COL1
CELL TYPE: DHS alpha
IMMEDIATE SOURCE:
CLONE: 97-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-474-633A-63
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0; Gaps
                                         1180 agtgaagaagaa 1191
                                                      70 AGAGAAGATGAA 8:
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1180 agtgaagaagaa 1191 || || || || || || ||

70 AGAGAAGATGAA 81

Search completed: May 29, 2002, 12:56:56 Job time: 9665 sec

| GenCore version 4.5 Copyright (c) 1993 - 2000 Compuges 1.td. | 29.6 26 0.5 25.4 0.5 | | MS9747 D.discoideu AR007403 Sequence AF025984 Paralicht AX033167 Sequence |
|--|--|---|--|
| OM nucleic * nucleic search, using sw model | 25,2 0.5 25,2 0.5 | 99 | AX033159 Sequence 165769 Sequence 5 |
| Run on: May 29, 2002, 09:42:16 ; Search time 5865,16 Seconds (without alignments) 17804 019 Million cell updates/sec | | 3 4 RABSFKHIB 2 6 AX173377 1 6 AR140801 1 6 193480 | M14473 Rabbit musc AX173377 Sequence AR140801 Sequence 193480 Sequence 78 |
| Title: US-09-676-436-3 Parfect score: 4990 Sequence: 1 ctagasasctctccgalgagctttatttaggaaggtc 4990 | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 6 195107 9 576509 3 UMOTRANSIN 5 AR007408 | 195107 Sequence 78 576509 D158 (A) (h L20950 Drosophila ARO07408 Sequence |
| Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 | 15 24 0.5 17 24 0.5 | 10 U92173 6 AX207310 9 A£04840511 | 592173 Mus musculu AX207310 Sequence ABG48411 Homo sapi |
| Searched: 1797656 seqs, 10463268293 residues | 24 00.5 | 6 AR014621 6 BD010413 | AR014621 Sequence BD010413 Chimeric |
| Total number of hits satisfying chosen parameters: 843946 | 23.8 0.5 | 4 AF29435455 | AF294358 Bos tauru |
| Minimum DB seq length; 0 Meximum DB seq length; 100 | 23.8 23.8 3.8 3.0 5.5 5.5 | 1 FRUITATC2 10 MW130784 | H28495 Trypanosoma |
| Post-processing: Minimum Match 04 Maximum Match 1004 Listing first 45 summaries | 23.8 0.5 23.8 0.5 23.8 0.5 23.8 0.5 | 6 AX326634 6 AX326671 9 S52152819 5 AFG25585 | AX326634 Sequence AX326671 Sequence SS2191 CD11b-1euko AF025985 Paralicht |
| Database : GenEmbl:* 1: qb_ba:* | 29 23.6 0.5 30 23.6 0.5 31 23.6 0.5 | 9 HSR305430 6 ARC62856 11 HUMUT770A | AJ305430 Homo sapi AR061856 Sequence L31186 Human STS U |
| 2: q0_nrq:* 3: q0_nr:* 4: q0_on:* | 23.6 0.5 23.6 0.5 23.6 0.5 | 6 AX326603 6 AX059502 5 AF025983 | AX124601 Sequence AX059602 Sequence AF025983 Paralicht |
| 5: 90.0v.* 6: 90.bat: 7: ab bat: | 23.4 | 6 A20455 10 RATPLYC 6 AX240922 | A20465 oligonucleo M32437 Ret/polyome AX240925 Geometre |
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| 10: 95_re. 10: 95_re. 11: 95_sts.* | 23.4 23.4 0.5 0.5 | 11 HSPE49C03 | ALO33823 H. sapiens M19461 Chicken C.B |
| 12: gb_sy:* 13: gb_un:* | 42 23 2 0.5 43 23.2 0.5 | 4 OCU72578 5 AP174523 | 072578 Oryctolagus AF174523 Bufo dana |
| 14: 9D_V1:* 15: am ba:* 16: em fur:* | 23 | 9 HSU32336 6 AR170294 | U32336 Human pre-B AR170294 Sequence |
| 17: en hum:* 18: en ln:* | | ALIGNMENTS | |
| 19: com_mu:* 20: com_mu:* | | | |
| | DOLOND DOLOND | 420 | 1001-004-7C /MT |
| | | ne, partial | |
| | VERSION MS9747.1 GI:167 | 7723 | |
| | SOURCE Dictyostelling di | iscoldeum (strain AX-3) DNA. | |
| | Sukaryota: Mycot | nschiusom tozoa; Dictyostellida; Dictyosi | tellum. |
| 31: en_ntg_cther:* 33: en_htg_cther:* 33: en_htgo_lnv:* | REFERENCE 1 (bases 1 to | 87) Dottin,R.P. of a protein kinase multigene i | family of |
| Fred. No. is the number of results predicted by chance to have a scote greatest than or equal to the score of the result being printed, and is derived by anyleis of the roral score distinctions. | Dictyostellum di CDNA encoding a JOURNAL Proc. Natl. Acad | Discreptelium discoldemm: Molecular cloning and expression of a CDNA encoding a developmentally regulated protein kinase perce Netl. Acad. Sci. U.S.A. 88, 1115-1119 (1991) | nd expression of a tein kinase 1991) |
| , | FEATURE SILVAILE LOCATION AND AND AND AND AND AND AND AND AND AN | Location/Qualifiers | |
| | | /organism="Dictyostellum discoideum" /elrain="Ax-3" | |
| No. Score Match Length DB ID Description | /db_xref. | ef-"taxon:44689" 87 | |

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BCT 21-SEP-2000
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GALCUSSER ANDREAS (DE): KRUE JOHANN (DE): LILL HELMUT (DE): STAHL PETER (DE): RRUGGER KERSTIN (DE): BORGYA ANNELIESE (DE): ROCHE DIAGNOSTICS GMBH (DE)
                   Actinopte.,
2 (bases 1 to 96)
2 (bases 1 to 96)
Quattro./ H. and Jones, W.J.
Quattro./ H. and Jones, W.J.
Direct Submission
Submitted (22-SEP-1997) Biological Sciences, University of South
Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA
Location/Qualifiers
1. 96
1. 96
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Amplification Primers That Target Locus-Specific Introns in Actinopterygian Fishes
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/allele="PdLDHA2"
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/db_xref="taxon:562"
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PdLDHA2, intron 6.
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1 (bases 1 to 100)
1 (bases 1 to 100)
Havelund, S., Ralatz.o slashed.m.J., Jonassen, E., Andersen, A. Sloth.
Havelunds, S., Ralatz.o slashed.m.J., Jonassen, E., Andersen, A. Acylataed insulin
Acylataed insulin
Patent: US 5750497-A 4 12-MAY-1998;
Patent: US 5750497-A 4 12-MAY-1998;
1. 100
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Perallchthys dentatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.

[ Loases 1 to 96]
Ouattro,J.M. and Jones,W.J.
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   /codon_start=1
/product="protein xinase 4"
/product="protein xinase 4"
/protein_id="Anx33189.1"
/db_xref="GT:167724"
/translation="NLIDOYGHIKLTDEGFARRITENTKSMC"
/ 1 2 c 1 4 9 25 t
                                                                                                                                                  Query Match 0.6%; Score 29.6; DB 3; Length 87; Best Local Similarity 59.5%; Pred. No. 1.8e+04; Matches 50; Conservative 0; Mismatches 34; Indels
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Sequence 4 from patent US 5750497.
AR007403 GI:3966887
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SOURCE ORGANISM synthetic construct.

ORGANISM synthetic construct.

ORGANISM synthetic construct.

ALTHORS HIGHS sequence.

ALTHORS ALTPRY AR. COLI'NS,P.L., Schmidt,A.C., Durbin.A.F.,

Skiadopoulos, M.H. and Tau.T.

TITLE Use of recombinant parainfilmense viruses (plvs) as vectors to prochest against infection and disease caused by pay and other human pathosens.

JOURNAL Parent: Mo 0142445-A 31 14-JUN-2001;

FRATURES

Local.Co.(Oublifitets)
Rabbit muscle phosptofruczokinase gene, exon 18.
MI4473 J 02/202
MI4473 I GI-165622
Phosphoryforutokinase.
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                                                                                                                                                                                 Dyacylois Michards Churdata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Lagomorpha; Laporidaes Oryctolagus.

1 (bases 1 to 03)

2 Enc. P. Rao, M. C., French. B. A., Putney, S. D. and Chang, S. H. The robbit musted the protein set cutture. Function and tissue specificity
protein structure. function and tissue specificity

3) Biol. Chem. 202, 4195-4199 (1987)

87166033

Dist entry and computer-readable sequence for [1] kindly provided by S. H.Chang, Oz. PEEP-1987.
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/db_xref="taxon:32030"
/note="Reverse primer for MSV A G gene insert"
3 12 c 26 g 34 t
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                                                                                                                                               Rabbit (New Zealand) DNA, clone lambda-Charon 4APFK.
Oryctolagus cunlculus
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/note="PFK intron R"
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16. .77
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                               linear PAT 21-SEP-200C
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1 (Dasse 1 to 70)

(Gallusser A. Korl, J. Lill, H., Stahl, P., Krucger, K. and Borgya, A. Merhod of identifying n-terminal probap
Peter: WO 04116-4 3 03-ADG-2000:
GALLUSER ANDRAS (CB.) * KRL JOHANN (CB.) : LILL HELMUT (DE) ;
STAHL PETER (DE) ; KRUEGER KENSTIN (DE) : BORGYA ANNELIESE (DE) ;
ROCHE DIAGNOSTICS GRBH (DP)

LOCALION/QUABILIEES
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Escherichia
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bb 2 AAACCCACTAAAGISAACTGTAACCGCATTTCGAATGAAGAGAGGGGT
2 AAACCCACTAAAGISAACTGTAACCGCATTTCGAATGAAGAGAAGGGATGAAGGG
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Best Local Similarity 54.3%; Pred. No. 2.88405;
Marches 51; Conservative 0; Mismarches 43; Indels 0; Gaps
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AUTHORS Neapher, R. B. and Summers, A.O.
TITLE Metal resistance sequences and transgenic plants
JOURNAL Patent: US 568294-A 5 16-5EP-1997;
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Sequence 5 from patent GS 5668294
165769 1 GI:2482339
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Sequence 1 from Patent W00045176.
AX031159
AX033159.1 GI:10280023
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                                                                                                                                 Escherichia coli.
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Unclassified.
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LOCUS 165769
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Query Match

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73 bp DNA Linear PRI 07-MAY-1993 DISS (A) [hypervariable minisatellite MS32] [human, individual MACH, Genomic, 73 nt].
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1 (Dases 1 to 73)
Monokton, DG, and Jeffreys, A.J.
Minisatallite 'Isoallele' discrimination in pseudohomozygotes by single molecule PCR and variant repeat mapping Genomics 11 (2), 465-467 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genbank staff at the National Library of Medicine created this entry (NCBI glbbsq 76509) from the original journal article. This sequence comes from Figure 2.
                                                                                                                                                                                                                                                                          0; Gaps
                                                                          1 (bases 1 to 71)
Toochmap,P.J., Kingquist,S. and Gold,L.
High affinity TGF beta, nucleic acid ligands and inhibitors Patent: US 5731424-A 78 24-MAR-1998:
                                                                                                                                                                                                                                                                                                      Oy 3958 gaacaigloathaggetglatteaaageagateaceattgegateaaegteetee 4012
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Gold,Lo., garl to 71)
Gold,L., Janjic,N. and Pagratis,N.
High affinity oligonucleotide ligands to growth factors
Patent: US 5207816-A 78 27 MAR-2001;
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Best Local Similarity 63.3%; Pred. No. 3.5e+05;
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Sequence 78 from patent US 5731424.
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Fri Jun 6 11:22:52 2003

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U92173 51 bp mkNA linear ROD :9-FEB-1998 Mus muscalus clone 103 T cell receptor beta chain mkNA, partial
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Eukaryota. Menaroa; Chordata. Craniata; Vertebrata. Euteleostomi;

Hammalia. Pinheria! Redectia. Sciucognathi; Muridae. Murinae. Hus.

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Johnston.S.L. and Metster...).

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minor histocompatibility antigens

1 / Menarot.

2 / Menarot.

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Direct Submission
Submitted (16-MRR-1997) Immunology, Mayo Clinic, 200 lst St S.W.,
Rochester, MN 55095, USA
Rochester, MN 55095, USA
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/strain=C5781s/6
/db.xtrai="taxon:10090"
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/col-type="Cylotoxic Tlymphocyte"
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120950, 120950, 121:104832
103050, 103050, 1031:104832
103050, 103050, 1031:104832
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SOUNCE
Drosophila melanogaster (individual_isolate 820.3) DNA.
REFERENCE
INDIVIDUAL DROSOPHILA D. M.
AUTHORS
ENGELS M. R. and Johnson-Schiltz.D. M.
TITLE Delta M. R. and Johnson-Schiltz.D. M.
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Sequence 9 from patent US 5750497.
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                                                                                                                                                     1736436 seqs, 858457221 residues
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                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          ON nucleic . nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT20934
AAC19445
AAC19445
AAAT2096
AAT22086
AAT22244
AAT32244
AAAZ3946
                                                                                                                            IDENTITY_NUC
Gapop.10.0 , Gapext 1.0
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Natch Length D
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44664444
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46844448
                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                  Database :
                                                                                                                                                      Searched:
                                                          Run on:
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Nucleic acid encoding p53-binding protein - which has homology to mouse Mdm2, for use in cancer research

Jochemsen A, Shvarts A, Van Der Eb AJ;

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They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                            AAQ86400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived from MRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyar RNAs derived from 30 different Lisaues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because thay are often obtained from oligo-dy primed cDNA identived from the STs are not vell suited for isolating cDNA sequences cDNA sequences have been obtained, the full 5' UTR is rarely included. ESTS ESTs are derived from mRNAs with included. S' ESTs are derived from mRNAs with included. S' ESTs are derived from mRNAs and genomic DNAs. 5' ESTs are also used used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruman: 5' EST; expressed sequence tag; sacreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                       1122 gtatgagggtgatgacacagaaggaggaattaaaggagttgggaaggtacggatgagag 1181
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' ESI) for obtaining CDNAs and genomic DNAs that correspond to 5'ESIs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                        The sequences of the 5' region (AAT50934) and 3' region (AAT50935) were deted. for cDNA clone 1, isolated from a mouse 16-day embryo. CDNA library using tumour suppressor p53 as probe. The 5' and 3' regions (AAT50936-37) of another clone were also detd. These sequences showed no significant homology to any known sequence submitted to several detabases. A third clone (see also AAT50933) coded for a p53 binding protein designated Mdmx (AAM10206).
                                                                                                                                                                                                                         ö
                                                                                                                                                                                          Query Match (1.5%; Score 27.2; DB 18; Length 78; Best Local Similarity 58.1%; Pred. No. 18+03; Natches 43; Conservative 2; Mismatches 29; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted, protein 5' EST, SEQ ID NO: 23520.
                                                                                                                                                  Sequence 78 BP; 33 A; 9 C; 22 G; 10 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 23520; 71pp + CD-ROM; English.
   Disclosure; Fig 2a; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAC19445 standard, cDNA; 92 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0122487
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                                                                                                                                                                                                                                                                                                                1182 tgoagaagaacaaa 1195
                                                                                                                                                                                                                                                                                                                                            61 tgvnghagacaaaa 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4469 asgeatgeagcotagtageatatggacttggaaeattctcttaetcectectgtatgtaa 4528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA086399 and AA086400 are a pair of primers for the PCR amplification of the Api3 B-Chain/Ala21 A-Chain human insulin derivative DRN. The two subunits of the derivative are covalently connected via disulphide bonds between Cys residues A7/87 and A20/819. The derivative, which may be present as a zinc ion complex, can be used as a fast action treatment for disbetes.
                                                                                                                                                                                            143 anamantquatgearcamatempeerecaecatumagacaetggmanneagtggagaatg 202
                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human insulin derivative; A-chain; diabetes; Zinc ion complex
Alazi PCR primer #128; ss.
                                                                                 Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Owery Match 0.5%, Score 26; DB 16; Length 100; Best Local Similarity 55:6%; Pred No. 27e+03; Matches 50; Conservative 0; Mignatches 40; Indels
                                                                          Ouery Match 0.5%; Score 26.6; DB 21; Length 92
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 36; Conservative 6; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acylated insulin deriv. which may be present as a line lon complex - is used to treat diabetes and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human insulin derivative Ala21 A-chain PCR primer #128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andersen AS, Halstrom JB, Havelund S. Jonassen I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 100 BP; 29 A; 22 C; 23 G; 26 T; 0 other;
Sequence 92 BP: 12 A: 9 C; 15 G; 47 T: 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1: Page 30; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ86400 standard; DNA; 100 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MO9507931-A.
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This invention describes a novel method to detect Niterainal pro-brain nattirutette privide (NP) in a sample using two antibodes, that recopiate districted privide (NP) in a sample using two antibodes. That recopiate districtions of the Niterainal pro-BMP. The method can be used for disquesting heart insufficiency. The recombinant in terminal pro-BMP is useful as a standard in a method to detect Niterainal pro-BMP and also for production of antibodies against Niterainal pro-BMP. This sequence represents a primer used in the cloning of recombinant recamainal pro-BMP and about the sample of recombinant this sequence represents a primer used in the cloning of recombinant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification of N'terminal pro-brain natifuretic peptide (pro-BNP) insing two antibodies that recognize different epitopes of line N'everminal pro-BNP, useful for diagnosts of best ansufficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene signature: messenyur RNA, mRNA: relative abundancu: frequency:
Furan: closing: mapping: vww.bised library: diagnosis; detection;
ccll typing: abnormal cc! lunction: ss.
                                                                                                                                   Brain natibrotic peptide: BNP, primer; human; detection; epitope;
heart; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Karl J, Lill H, Stahl P. Krueger K, Borgya A, Gallusser A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oucry Match

O.51: SCORE 25.2: DB 21: Length 70:
Perf Local Similarity b.29: Pred: No. 3.7e-03.
Berches 39. Conservative C. Mismatches 23. Indets (
                                                                      Human brain matriaretic peptide N-terminal primer Pro2hum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOFF ) ROCHE DIAGNOSTICS GREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-2000: 2000WO-EP00632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-1999: 99DE-1003439.
12-MAR-1999; 99DF-1011044
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    11-DEC-2000 (tirst entry)
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                                                                                                                                                                                                                                             Homo Saptens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel use for sequence variants of the human particular physiological and particular particula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human: G-protein subunit Gbetal; variant; high blood pressure; asthma, hyportoola; cardiac infarction; coronary disease; heart disease; troubition disease; dabetee; psychiatric disease; Crohn's disease; tambunological disease; psoriasis; colitis ulcerosa; transplant rejection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use of sequence variants of the beal subunit of human G prouein re
predict, detect, and deteratine drug targets for diseases including
heart, immological and psychiatric diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 0.5%: Score 25.2; DB 22; Length 60; Local Similarity 66.7%; Pred. No. 3.4e+03; ess 36; Conservative 0; Mismatches 18; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human G-protein subunit Sbeta3 intron 9 DNA fragment $2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 60 BP: 6 A; 11 C; 6 G; 37 T; 0 other;
4529 tatttacataaagactgtgctgagaagcag 4558
                                                                 37 CANTIGGARACTACTGTGCTTAGACGCAG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure: Page 3; 14pp; German.
                                                                                                                                                                  ARESULT 4
AM148689:

AM448689:

AM448689:

XX AM448689:

XX I 9-OCT-2001 (first entry)

XX I Wann G-protein subunit obeta3 in

XX I Wann G-protein gases; dabetes; ps

XX I Wann G-protein disease; dabetes; ps

XX I Wann G-protein disease; dabetes; ps

XX I WAC-2001.

XX I DE-2000; 2000DE-1007687.

XX I WA G-1FP/) SIFFERT W.

XX I SI
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ID AAA71594 etandard; DNA: 70 BP.
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NC AAA71594;
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Best Loca Matches

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0: Gaps

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Organometal; resistance; transcription; translation; regulation; merA; transposon; Toll; merB; mercuric ion reductase; organomercury lysse; ss: transgenic plant; detoxification; meral compound; soil; sediment; priner; aquatic environment; bioremediation; contramination; PCR; amplification.
                                                                                                                                                                                                                                                                                                                                      The present sequence represents a PCR mutagenesis primer used to mutagenise the merA coding sequence derived from transposon Infl., to adapt it for plant expressibility. The nucleic acid molecule produced is useful for producing transpenic plants that are reasistant to toxic heavy netals (especially mercury) and so can be used remediate and/or revegetate contaminated areas. The bacterial merA gene is derived from the transposon Inl., which was originally isolated from the Incompatibility Group IncFII resistance plasmid NRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3026 atgtcctgactaatgtgagagtggtagaggtbcaagacccaggtgggcgactcaaggat 3085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 magacccmgctataggigangctgttactgctgcatttcgcatgganggcattgmagtgc 61
                                                                                                                                                                                                                           DNA encoding marcuric ion reductase in plant-expressible form · for producing transgenic plants resistant to toxic heavy metals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 0.5%; Score 25.2; DB 18; Length 99; Best Local Similarity 54.3%; Pred. No. 4.78+03; Matches 51; Conservative 0: Mismatches 43; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Column 43-44; 52pp; English.
                                                                                      (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer 307-339S for In21 merA gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA228594 Standard; DNA; 99 BP
                                              95US-0427097.
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  950S-0427097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-1999 (first entry)
                                                                                                                                       Summers AO;
                                                                                                                                                                                 WPI: 1997-470112/43
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Transposon Tn21.
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21-APR-1995;
                                         21-APR-1995;
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                                                                                                                                       Meagher RB,
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  #X#X#X#X####X###X
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 '62' sequences of given in AAT19001-T2683 and which is able to hybridise to part of given in AAT19001-T2683 and which is able to hybridise to part of human genomic DNA. CDNA on mRNA is claimed. The GS (Gere Signature) sequences were obtained from a 'directed DDNA libraries prepared from various human tissues; synthesis of CDNA was inliated from the CS '-end of mRNA by using poly(T) as the sole primer. Since the 3'-outsansisted cobna, hybridise with specific mRNAs. Each library CS all the 3'-oriented cobna, hybridise with specific mRNAs. Each library of is constructed cobna, hybridise with specific mRNAs. Each library of afferent mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. waling primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4485 agamtatggmettggmmmattctcttmmtcmctactgtatgtmatatttmcmtmagmet 4544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRMA in specific human tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.5%; Score 25.2; DB 16; Length 89; Best Local Similarity 62.9%; Pred. No. 4.4e+03; Antiches 39; Conservative 0; Mismatches 23; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metal ion resistance; mercuric ion reductase; merk; mercury; toxic heavy metal: transgenic plant; mutagenic; bacterial; transposon; Tn2l; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mercuric ion reductase merA PCR mutagenesis primer 307-339S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 89 BP; 39 A; 8 C; 15 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1039; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT92244 standard; DNA; 99 BP.
                                              94WO-JP01916
                                                                                      93JP-0355504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JAN-1998 (first entry)
                                                                                                                                                                                                      Matsubara K, Okubo K;
                                                                                                                                  (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                  WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Transposon Tn21.
                                            11-NOV-1994;
                                                                                        12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4545 gt 4546
01-JUN-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
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Metal resistance sequences for producing transgenic plants .

Summers AO;

Meagher RB,

WPI; 1999-579950/49.

USS668294-A.

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16-SEP-1997

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Gaps

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                                                The invention relates to a nucleic acid molecule comprising a coding asquance for an organometal resistance protein, which is operably it asquance for an organometal resistance protein, which is operably in linked downstream of and under the regulatory control of a control of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a primer used to generate a synthetic of p gene by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           betermining translational efficiency of codons in cells, comprising introducing synthetic constructs with reporter genes (used in frame to tandem repeats of the codon, and measuring expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3026 atgiccigacianaigigagagiggiagaggiacaagacccaggiggggactcaaggal 3085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:

0.51, Score 25.2; DB 20; Length 99;

Best Local Similarity 54.31, Pred. No. 4.7e+01.

Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 magaccomgetataggtgaagetgttactgetgeatttegeatgguaggeattgamgtge 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green fluorescent prolein; GFP; reporter gene; codon utilisation; translational efficiency; protein abundance; PCR primer: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3086 ttgattttctacaagcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Column 17-18; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1, Page 183, 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANA 3946 standard; DMA; 54 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFP Leu(CTG)5 forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2000; 2000MO-AU00008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JAN-1999; 99AU-0008078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UTQU ) UNIV QUEENSLAND. (SUNX/) SUN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 2000-499118/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou J. Frazer IH;
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CCR amplification of a humanised gfp gene. A single artificial start codon followed by a streeth of five identical codons was fused in frame codon followed by a streeth of five identical codons ask fused in frame immediately upstroam of a cip codding sequence to form the synthetic gene. The applified fragment was clored into the mainmallan expression vector probabilitied fragment was introduced to the general used in a cell. The synthetic construct was introduced into toos it a codon in a cell. The synthetic construct was introduced into toos it as according to frame by a tandem fright of the gip gene is preceded to frame by a tandem fright of the gip gene is preceded to frame by a tandem friend to a factical codons with a higher central efficiency than their corresponding synonymous codons can be facted codons may then be used to replace the less preferred codons and the protein expression with an undifferentiated epithelial cells such as COS-1 cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human: foetal liver; gene expression; single exon nucleic acid probe: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for beauting human forter. In seasing human forter and in a sangle desired from human forter. If the single exon nucleic acid probes may be used for predicting magnified and displaying one expression in samples derived from luman feets live present sequence is a single exon nucleic acid luman probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

D.51: Score 25; DD 21; Length 54:
Rest Local Smilarily 59:44; Pred. No. 3:6e-02;
Matches 34; Conservative 5; Mismatches 15; Indels D: Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4, SEQ ID NO 17996; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human foetal liver sludle exon nucleic acid probe #17996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54 BP; 9 A: 14 C: 20 G: 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG, Hanzel DK, Cher. W. Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000; 2000US-3207456.
93-UM-72000; 2000US-06646.
03-ARG-2000; 2000US-053366.
21-SBP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA69691/c
ID ABA69691 standard: DNA, 91 RP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001MO-US00669.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens.
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26-MAY - 2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences.
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Sequence 91 BP; 28 A; 19 C; 13 G; 31 T; 0 other;

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3815 acquattgaasatattcgaaggcatcaaacaccccaatctggtcggtattttggtgtgg 3874
                                                  0; Gaps
                                                                                                                       67 ANGANATTATTATGATGANGACTGTANACCCCANATATTGTTGCTTATTTTGGANGCT 8
Query Match 0.5%; Score 25; DB 22; Length 91; Best Local Similarity 61.5%; Pred. No. 5.1e+03; Matches 40; Conservative 0; Mismatches 25; Indels
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7 ATCTC 3 a

Human secreted protein 5' EST, SEQ ID NO: 16467.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosoma mapping; ss.

Dumas Milne Edwards J, Duclert A, Giordano J;

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

Isolated infectious chimeric parainfluenza virus (PIV), useful in an attenuated vaccine to elicits an immune response against one or more virus(es) selected from human PIVI (HPIVI), HPIV2 and HPIVI -

Claim 1; SEQ ID 16467; 71pp + CD-ROM; English

The present sequence is one of a large number of 5' ESTs derived from manks encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polya+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslabated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA. Ilbraries. Such ESTs are not well suited for isolating cONA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length CDNAs and genomic DNNs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. RESULT 11

AAC12392,

AC12392,

AC12392;

AC12392;

XX

AC12392;

XX

DE AAC12392;

XX

Human secreted protein 5' E5T, SEC

XX

KN

Human; 5' E5T; expressed sequence

XN

Human; 5' E5T; expressed sequence

XX

Homo sapiens.

XX

Homo sapiens.

BP1033401-A2.

XX

AX

CESP-2000;

XX

CESP-2000;

XX

AX

AX

CESP-2000;

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CESP-2000;

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CESP-2000;

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CESP-2000;

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CESP-2000;

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CESP-2000;

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CESP-2000;

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CESP-2000;

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CESP-2000;

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CESP-2000;

AX

AN

WPI: 2000-500381/A5.

PT

Dumas Milne Edwards J, Duclert A

AX

WPI: 2000-500381/A5.

PT

Dumas Milne Edwards J, Duclert A

AX

WPI: 2000-500381/A5.

PT

CLand I, SEQ ID 16467; 71pp + CD
XX

CESP-2000;

CERPICATE AND AS

CE CAPA Sequences usually correspond main

CE CHO human NAMS or poly4+ RNAS of

CE CHO COPEAN (full length CDNAS)

CE COPEAN (full length CDNAS)

CE COPEAN (full length CDNAS)

CE USA Sequences have been obtained

CE COPEAN (full length CDNAS)

CE USA Sequences have been obtained

CE COPEAN (full length CDNAS)

CE USA Sequences obtain (full length CDNAS

CE USA Sequences (COPEAN)

CE USA Sequence AT BP; 27 A; 14 C; 15 G;

Sequence 77 BP; 27 A; 14 C; 15 G; expression and secretion vectors.

Sequence 77 BP; 27 A; 14 C; 15 G; 21 T; 0 other;

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                                                                                                               Infectious chimeric parainfluenza virus; antigenic determinant: nuclaecepsid phosphoprotein; large polymerase; attenuated vacchne; human prvi; HPV1: HPV2; RPV3; RSV; pathogen; mesales; PCR primer: respiratory syncytial virus; respiratory tract infection; bovine; fs.
                                                           O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murphy BR, Collins PL, Schmidt AC, Durbin AP, Skladopoulos MH:
Tao T;
0.5%; Score 24.8; DB 21; Length 77:
60.3%; Pred. No. 5.2e+03;
iive 0; Mismatches 27; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reverse PCR primer for RSV A G gene insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                        AASO66310 standard; DNA: 92 BP.

AASO6630.

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AASO6930:

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AASO6930:

XX
AASO6930:

XX
AASO6930:

XX
AASO6930:

XX
Infectious chimeric parainfluenza
MW inclacocepsid phosphoprorecten; large
MW muclacocepsid phosphoprorecten; large
MW muclacocepsid phosphoprorecten; large
MW muclacocepsid processor
XX
HWAAA (ESPIZATA)
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HWAAA (ESPIZATACY SYNCYLIAI VITUS; respi
XX
HWAAA (ESPIZATACA)
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HWAAA (ESPIZATACY SYNCYLIAI VITUS;
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HWAAA (ESPIZATACY SYNCYLIAI VITUS;
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HWAAA (ESPIZATACY SYNCYLIAI VITUS;
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HWAAA (ESPIZATACA)
XX
HWAPH BR, COILINS PL, Schmidt PR
MY (ESH) US DEPT HEALTH & HUWAN SER
XX
HUTPHY BR, COILINS PL, Schmidt PR
TAO T;
XX
HATCHILLS (ESPIZATACA)
XX
TACA (USSH) US DEPT HEALTH & HUWAN SER
XX
WPI; 2001-156173/37.
XX
EXAMPLE 10; Page 150; 305pp; Englist
XX
WPI; 2001-156173/37.
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EXAMPLE 10; Page 150; 305pp; Englist
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WPI; 2001-156173/37.
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EXAMPLE 10; Page 150; 305pp; Englist
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CC (AASO6939) in the construction of
XX
CC (AASO6939) in the con
   Query Match 0.5
Best Local Similarity 60.3
Matches 41; Conservative
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The present sequence for reverse PCR primer for respiratory syncytial vire present sequence for reverse PCR primer (RNY) A G gene insert is used with the forward PCR primer (AAS06929) in the construction of boving-humanPlV3-RSV chimeric viruses. The sequence is described in an invention relating to novel infectious chimeric parafilluanza viruses (PIVS). The virus complete PV weren infectious cultimorable protein (I), and a partial or complete PIV vector background genome, or antigenome combined with one or more berechologous gene(s) or genome segment(s) encoding one or more antigenic determinants of one or more heterologous pathogen(s) to form a chimeric genome or antigenome or more witue(es) selected from human privi (HPIVI), HPIVZ and HPIVZ and segment(s) to form a chimeric genome or antigenome craphogen(s) to form a chimeric piv is useful in an attenuated vaccine to elicit an immune response against HPIV3, measles or RSV. An immunospecific composition may also contain two chimeric PIVW, where the first chimeric HPIVI) may also elicit a polyspecific immune casponse against HPIVI and the second chimeric PIV elicits and immune response against HPIVI and HPIVZ and where both the first and second chimeric PIVE ellicit and immune response against HPIVI and immune response against Example 10; Page 150; 305pp; English.

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Human: 5' FST; expressed sequence tag; socreted protein; cDNA isolation; gene therapy; c/romosome mapping: 5s.
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2 gamaatataaaaalactaancaaaagaaqtetgagglaactutggfaatattaaaactec 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein 5' EST, SEQ ID No: 19616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duras Milne Edwards J, Duclert A, Giordano J:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clain '; SEQ ID 19616: 71pp + CD-RCM: English.
                                                                             1439 acaagctastagatagtteetsucaaaggges 1476
                                                                                                                                                      52 angatttastglaggaddtattattsasggra 93
                                                                                                                                                                                                                                                                                                            AAC15541/c
ID AAC15541 standard: cDKA: 94 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2000: 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-007 2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2030-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMU Saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAC15541
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     8
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                                                                                                                                                                                                                                                                        :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, 5' EST; expressed sequence tag: secreted protein; cDNA inclation;
gene therapy; chromosome mapping: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed equence tag (5' EST) for obtaining CBMs and Genomic DMs that correspond to 5' EST, and (io obtaining CBMs and demonster to Cression and CBMs that act of the consense mapping procedures .
                                                                                                                                                                                                                                                                                                                                                     Query Match 0.5%: Score 24.8; DB 22; Length 92; Best Local Similarity 63.3%: Pred. mo. 5.9%-02; Indels C: Gaps Matches 38; Conservative 0; Missatches 22; Indels C: Gaps
                                                                        Sequence 92 BP; 20 A: 12 C; 26 G; 34 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein 5' BST, SEQ TD NO: 15574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 94 BP: 46 A; 9 C; 14 G; 25 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J. Duclert A. Giordago J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 15574; 71pp + CD-ROM: English.
          particularly in young children.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC11499 standard: CDNA: 94 RP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-1999; 99US-0122487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-0CT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1033401-A2.
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ACTIA199

ACTIA1

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the present sequence is one of a large number of 5' ESTs derived from ranks encoding secret proteins. No ONE has yet been conclusively of control than 10 by the present sequence. The 5' ESTs were prepared from the control human Rha or polyar Rhad edrived from 10 different tissues. ESTs control human Rha or polyar Rhad edrived from 10 different tissues ESTs control from 10 to 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 94 BP: 35 A: 10 C: 29 G: 16 T, 4 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1655 tetach 1650
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Query Mutch 0.51; Score 34.8; DB 21; Length 94; Baset Local Similarity 54.34; Pred. No. 5e-03; Index 50; Conservative 0; Maratches 42; Indexs 0; Caps

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The present sequence, a transforming growth factor beta-1
C (TGF-beta-1) binding ligand, was identified by Systematic Evolution
C (TGF-beta-1) binding ligand, was identified by Systematic Evolution
C filgands by Exponential enrichment (SEEX). Briefly a candidate
mixture of nucleic acids was contacted with TGF-beta-1, and nucleic
C acids having an increased of filiaty to TGF-beta-1 partitioned from
the remainder of the mixture. The partitioned nucleic acids were
then amplified to yield a mixture of nucleic acids enriched for
C sequences with higher affirity and specificity for binding to
C TGF-beta-1. The ligand is anti-mitogenic and may be used to inhibit
E TGF-beta-1 mediated pathological conditions, e.g. fibrotic
C conditions such as fibroids of the kidney, lung and liver and more
c acute conditions such as dermal scarring and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification of nucleic acid ligands to TGF-beta, PDCF and hKGF using SELEX, used in the diagnosis and treatment of proliferative disorders
                                                                                                                                                                    Transforming; growth factor; beta-1; TGF-beta-1; binding ligand; identification; SELEX; anti-mitogenic; inhibition; cell; systematic Fvolution of Ligands by Exponential enrichment; epithelial; proliferation; diagnosis; trastment; fibroids; kidney; lung; liver; dermal scarring; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sold L, Janjic N, Pagratis N, Ringquist S, Toothman PJ;
                                                                                                                                        Transforming growth factor beta-1 binding ligand D 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 71 BP; 15 A; 16 C; 22 G; 18 T; 0 other;
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ö 0; Gaps Ouery Match 0.54; Score 24.6; DB 18; Length 71; Best Local Similarity 65.54; Pred. No. 5.7e+03; Matches 16; Conservative 0; Mismatches 19; Indels 0

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Search completed: May 29, 2002, 13:05:25 Job time: 9833 sec

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| | Gencore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. | | مممد | 2220 | r62011 81858071 8H127075 | T62011 yb97b12.rl BT856071 603384887 BH127076 G-10924.f AAR65746 CH41h11 4 |
|---|--|--|--|--|--|--|
| OM nucleic - r | nucleic search, using sw model | | 600 | 00 | 51245 35450 | AT251245 qv55912.x AT235450 ub47b05.r |
| Run on: | May 29, 2002, 09:13:38; Search time 35:8.59 Seconds (Without allyments) 19141,135 Million cell updates/sec | 0 | an a a | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | 1089/ 40694 94187 62956 | A1340694 th53c05.x A1340694 th53c05.x A1894187 mc67c06.x A1142956 ox58d01.x |
| Title: Perfect score: Sequence: | US-09-676-436-3 : 4990 : ctagaagacttctccgatgaggtttatttaggaaagric 4996 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 255.6 225.4 255.4 255.4 255.4 255.6 255.6 255.6 | 85 9 AV5 70 9 AV5 89 12 AX1 | A10863/8 AV532477 AW149995 A2961698 | AVS52477 AVS52477 AVS52477 AVS52477 AVS5265 AGS5265.x AZ961658 2M0230B17 |
| Scoring table: | : IDENTITY_MUC Gapop 10.0 , Gapext 1.0 | 7 M 47 | ခ်စ်စ် | 275 | C19910 AF149669 AA669624 | AF149669 AF149669 AF1669524 AC20AQ2.8 |
| Searched: | 13736207 \$8qs, 6748477542 residues | | စ်စစ် | 200 | ALBS2095 AAS76542 BG362475 | AL662095 AL662095 AA576542 DM66c06.8 BG362479 qb73a06.v |
| Total number o | of hits satisfying chosen parameters: 297742 | 60 U | ن ن | 20 | 054677 | BE054677 7169e05.y |
| Minimum DB 86c | <pre>seq length: 0 seq length: 100</pre> | 60 T | 9 9 9 6 | 6 - 6 | AZ574215 AZ574215 AA451873 | AZ574215 326PV808 AA451873 XX16e01.8 |
| Post-processi | Poet-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries | V 5 | 5000 | ,222 ,222 | A1339161 C01741 B1943038 TA330B01P | A139404 quinquix C01741 HUMCSO00363 B1943038 SH03504.9 AL492:49 T. brucei |
| Pred Wo. score greed and 19 26 4 4 28 6 6 27 8 6 6 27 8 6 6 27 8 6 6 6 27 8 6 6 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 | edicted by chargone of the results in score distributions. | RESULI AA990067 AA990067 LOCUS INCLESTON RESTON REPRESONS REFERENCE SOURCE ORGANIS TITLE JOURNAL COMMENT COMME | c | ALIGNMEN MA990067 Da556102.T1 Scares_thymus_JabbyT M HMACE:13616915', mRNA sequence. AA990057.1 GT:3175431 AA990057.1 GT:3175431 Couse mouse. MA990067.1 GT:3175431 Couse mouse. MA990067.1 GT:3175431 Couse mouse. MANDAIN MACEZOA: Clordote; CT: Wammala: Fitheria: Rodentia; Sc MATEAN. Hilleri. A'lcn, M. I Schellecherg, K., Steptoc, M., Tar, MAHESIAG, B., Myller, T., Lennon.G. AABAGESTOR. MAHESIAG. B., Myller, T., Lennon.G. MAHESIAG. B., MYLLER, MYL | ALIGNMENTS AUGUNETTS AUGUNETTS AUGUNETTS ANGOOGT ANG | ALIGNMENTS ALIGNMENTS ALIGNMENTS Specifications and the sequence. AA990067 AA900067 AA9000 |

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Tumor Gene Index

(Depublished (1997)

Transport Strawberg, ph.D.

Email: cgapbs-remail.nih.gov

Trasue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Email: cgapbs-remail.nih.gov

Trasue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Gencem

Clone distribution: NCI-CGAP clone distribution information can before distribution; NCI-CGAP clone distribution information can before distribution; NCI-CGAP clone distribution information can before distribution information can be found distribution information can be conditioned distribution can be conditioned distributioned distribution can be conditioned distributioned distributioned distributi
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Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZhBM), pregnate uterus whithy, and fetal heart NDHAIDW) were made in vitro. Following HAP purification, this DNA was used as traces in a subtractive hybridization on reaction. The driver was PCR-amplified cobMas from pools 5,000 clones made from the same 3 libraries. The pools consisted of 1 M.A.G.E. clones 260232-265223, and 484468-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1767078 11.0EC.1999 A1892.34012 Homo sapiens CDNA clone IMAGE: 2400828 3',
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Eukaryota, Hetazoa: Chordata: Cranlata: Vertebrata: Euteleostomi;
Homanalla: Eutheria: Prinates: Catarrhini; Hominidae: Homo.
1. (bases 1 to 71)
MCT-CGAP http://www.ncbl.nlm.nlh.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/tissue_lype="? pooled tumors (clear cell type)"
/lab_host="DH100"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%; Score 29; DB 9; Length 70; Best Local Similarity 71.7%; Pred. No. 1.4e+04; Matches 38; Conservative 0; Mismatches 15; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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16 c
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AI757078
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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1 (basea 1 to 70)

1 (basea 1 to 70)

1 (basea 1 to 70)

2 (basea 1 to 70)

3 (basebar, Lacy, M., Le, M., Le, M., Le, M., Marra, M., Martin, J., Woore, B., Schellenborg, K., Steplee, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R.

4 (bashib-Merck Est Project 1997)

4 (bright)

4 (bright)

5 (contact: Wilson RX

6 (bashiband (1997)

6 (contact: Wilson RX

7 (bright)

7 (contact: Wilson RX

8 (bashiband (1997)

8 (bashiband (
                                                                                                                    Anote—"West only prilibrac (Pharmacia) with a modified polylinker; Sited.: Not II: Site_2: Eco Rr; ist strand CDNA was primed with a Not I - oligo(dI) primer [5' double-stranded CDNA was lighted to Eco RI adaptors 3'; double-stranded CDNA was lighted to Eco RI adaptors and Eco RI sites of the modified prira and cloned into the Not I and Eco RI sites of the modified prira vector. RNA provided by Dr. Bertrand Jordan . Library went through two Founds of cornalization, and was constructed by Bento Soares and M.Fitima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA490364 70 bp mRNA linear EST 08-AUG-1997 aa44cl0.rl Scares_NhHMPu_S1 Homo sapiens CDNA clone IMAGE:823794 5' similar to SW:NIM1_NEUCR P48479 PROTEIN KINASE NIM-1; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:823794"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watch 0.8%; Score 39.8; DB 9; Length 95; Local Similarity 70.7%; Pred. No. 24; conservative 0; Mismatches 22; Indeis
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1. .70
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/lab_host-"DH105"
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AA490364.1 GI:2219537
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a õ 8 us-09-676-436-3.szlm100.rst

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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Cloud Library Mashington University Genome Sequencing Center
Cloud Library Library I.M.A.G.E. Consort Implied at:
Mr.A.G.E. Consort Implied at:
Mr.A.G.E. Consort Implied at:
Mr.A.G.E. Distance 11 Library Library Library Library Library Library Sed Primer:
Mr.A.G.E. Consort Library Sequence Stop: 76.
Migh quality sequence Stop: 76.
Localion/Ontalifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI122285 94 bp mRNA linear EST 30-JUL-2001 XX15a08.y3 Parastronqyloides trichosuri fu pAMP1 vl Chiapelli MCCarter Parastrongyloides trichosuri cDNA 5', mRNA sequence. BI122285
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Parastrongyloidus trithosari.
Parastrongyloidus trithosari.
Dukaryota: Maczoa, Mematoda: Chromadorea: Rhahdllida:
Paragrolainoidea: Strongyloididae; Parastrongyloides.
1 (bases: Lo 94)
McCarterij, Cifton, S., Chiapoili, B., Pape, D., Martin, J., Wylle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Dowers, Y.
Homo sapiens
Eukarycka, Metazoa; Chordata; Craniata; Verlehrata; Fute; eostomi;
Mammalia; Eutheria primates; Catarthini; Hominidae; Homo.
(bases 1 to 81)
VCI/NINDS-CGAP http://www.ncbl.im.nlh.gov/nchcgap.
NCI/NINDS-CGAP http://www.ncbl.im.nlh.gov/nchcgap.
Disorders and Stroke, Bial.n Timor Genume Anatomy Project
(CGAP) PRCARP). There Gene Index
Unpublished (1998)
Contact: Rober: Strauberg, Ph.D.
Email: capabs-refmail.oih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O: Caps
                                                                                                                                                                                                                                                                                           CONA Library Preparation: M. Bento Soares, Ph.D., M. Falima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="1MAGE:2019185"
/clone="1h="VicCobp_Brn25"
/lissuc_Lype="anaplastic oligodendroglioms"
//ab_host="0H108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 27.8; DB 9; Length 83; 59.5%; Pred. No. 3e+04; tive 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Homo sapiens"
/db_xref-"taxon:9606"
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                                                                                                                                                                                                                                                                                                        83 bp mRNA linear EST 07-PEC-2001 BJ06432 NTBB Mochil normalized Xenopus tailbud inbrary Xenopus Jaevis CRN clone XL076el3 5', mRNA Sequence. BJ063432 BJ063432 GI:17424723 EST 05 BJ063432.1 GI:17424723
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DEFINITION qy99d09.x1 NCI_CGAP_Brn25 Homo sapiens CDKA clone IMAGE:2019185 3',
MRNA sequence.
ACCESSION AI360096
AI360096.1 GI:4111717
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Amphibia; Botrachia; Anura; Mesobatrachia; Pipoiden; Pipidae;
Xenopodinae; Xenopus,
1 (bases 1 to 83)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
                                                                                   135 tttgaaagaaatgaatgcaccaaatcaycctccacataaaqocactggaaaaacagt 194
Objety Match 71;

9.6%; Score 28.6; DB 9; Length 71;

Best Local Similarity 64,2%; Pred. No. 1,76+04;

Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tadasu SAIn-1
Centear: Por denetic Resource Information
National Institute of Genetics
1111 Yata, Mishina, Shizuoka 411-8540, Japan
Tel: 811-559-81-6655
Par: 81-559-81-6655
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/dev_stage="stage 25"
15 a ll c ll g 42 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL076e13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tshinifgenes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 African clawed frog.
Xenopus lasvis
                                                                                                                                                                            Oy 3145 ttgagtt 3151
                                                                                                                                                                                                                  62 TIGATIT 68
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A1360096/c
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BJ063432/c
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TITLE JOURNAL COMMENT

PEATURES

us-09-676-436-3.szlm100.rst

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/Issue_type="Thymus"
/dev_stage="4 weeks"
/dev_stage="4 weeks"
/lab_lost="Data"
/laba"
/l
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Waterston, R.
The Wash HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
Washu-HMI Mouse EST Project
Washu-HMI Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of NedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
742: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Fhis olone is available royalty'free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:357862
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1 (basea 1 to 91)
Hillier L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Riffin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Materston, R., Williamson, A., Wohldmann, P. and Milson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3977 atteasageagateaceattgegateaaegteeteeatgageatggeatagteecegtg 4036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality
Trace considered clone: similarity on wrong strand
Seq priner: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref-^tcaxon:10090*
/clone-_TyAGE:583214*
/clone_lib-*Soares_thymus_2NbMT*
/sex-*male*

    100.
    organism="Mus musculus"
    strain="C57BL/6J"

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185845/c
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The Mashington Univ. Nematode EST Project, 1999
Contact: Mocarter 1999
Washington University School of Medicine
(444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 316 286 1800
Fax: 316 286 1800
Fax: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ander-Vector: pAMP1 (Gibco): Site_1: Not1; Site_2: Sall:
The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
CDNA was made by using Dynabead oilgo-dr priming (Dynabead oilgo-dr priming (Dynabead oilgo-dr priming (Dynabead oilgrary using a modified protocol from the
SNART PCR CDNA Syrthesis Kit from Clontech. Directionally
cloned into the UDG sites of pAMP1. Nemtodes were
provided by Dr. Warwick Grant of Agrearch, New Zealand
(warwick, grant@agresearch.co.nz).*
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AALS4655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus

Rukaryota: Metazoa; Chordata; Craniata: Vartebrata; Euteleoslomi;

Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae: Murinae; Nus.

1 (Dases I to 100)

Marra, M., Millier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, M., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylle, T., Lennon, G., Soares, B., Milson, R. and
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     dibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronkoji, Kennedy, S., Maguirei, Beck., Underwood, K., Steptoe, M., Allen, M., Person, B., Svaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardens, M., McCann, R., Waterston, R. and
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Expression map of the C.elegans genome
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Nettoned Institute of Genetics
Yatu 1111. Mishins. Shizuoka 411. Japan Tel: 81-559-81-0854
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Location/Qualifiers
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Contact: Hilson R.

Mashington University School of Medicine
4444 Forest Park Barkway, Box 850;, St. Louis, MC 51:08

Tel: 314 286 1800

Enail: 6246 4800 Mustl.edu

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Bukaryota Hetatoda Chordata; Catarrhini, Hominidae. Homo.
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MCI-CGAP http://www.ncbi.nim.nih.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Local Similarity 54.44: Pred. No. 319e-04.
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Contact: Robert Strausberg, Ph.D.

Contact: Robe
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/lab_host="DH10R"
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RS MIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Deffrey Green M.D.
CONTACT, Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Close distribution: MGC clone distribution information can be found through tha I.M.A.G.E. Consortium/LINL at:
http://mage.lln.gov
Plate: LubM8933 row: m column: 10
High quality sequence Stop: 81.
Location/Qualifiers
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/strain="FVN"
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/lab_host="DH108"
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/OD_XTES-"taxon.0506
/OD_XTES-"taxon.0506
/Clone="INACE:1588653"
/Clone="INACE:1588653"
/LISSUE_TYPE="Z_POOLEd tumors (clear cell type)"
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Schellechary, R., Steptoo, M., Ten. M., Wattin. Morris. M.,
Schellechary, R., Steptoo, M., Ten. M., Underwood, R., Morres. M.,
Mattaing, M., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
Materiaton, R.
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ORIGIN
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AUTHORS
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AUTHORS
TITLE
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Email: W-Saber@FRCU.EUN.DC
Seq primer: 8k.
Location/Qualifiers
1. 050
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Location="Expression mansoni"
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ပ် Query Match

0.5%; Score 26.4; DB 10; Length 95;
Best Local Similarity 59.2%; Pred. No. 7.3e+04;
Matches 45; Conservative 0; Mismatches 31; Indels 0; Gaps

701 tcamagtcgmctmtgg 716 | | | | | | | | | | 65 TGAMATTTACCATAG 80

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Search completed: May 29, 2002, 11:17:02 Job time: 7404 sec

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SESULT 1

SEGURE 4. Application US/08400256

SEGURECAT 1. Application US/08400256

SEGURECAT: HOUSEWAYTURE

SEGUREAL NO. 5750497

APPLICANT: HAISTURN 30::
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APPLICANT: Accesser, Asset Sloth
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                                           Sequence 260
Sequence 260
Sequence 360
Sequence 39, Asparance 19, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 11, Sequence
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                 Sequence
US-D8-465-5914-75
US-D8-465-594A-75
US-D8-973-124-250
US-D8-08-08014-260
US-D8-488-122-99
US-D8-110-286A-39
US-D8-110-286A-39
US-D8-41-59-40-31
US-D9-41-59-51
US-D9-41-39-63-55
US-D8-445-464C-10
VS-D8-60Z-093-23
US-D8-60Z-093-23
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US-D8-60Z-093-23
        TOPOLOGY: TINEST NOLECULE TYPE: DNA US-08-400-256-4
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                                                                                                                                                                                                                                    May 29, 2002, 10:15:51; Search time 94.14 Seconds (Without alignments) 13020.089 Million cell updates/sec
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4990
1 Cragaagacttctccgatga.......ggtttattttaggaaagctc 4990
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1: /cqn2_E/ptodata/1/ina/5A_COMB.seq:

2: /cqn2_E/ptodata/1/ina/5B_COMB.seq:

1: /cqn2_E/ptodata/1/ina/6A_COMB.seq:

4: /cqn2_E/ptodata/1/ina/8E_COMB.seq:

5: /cqn2_E/ptodata/1/ina/ba_COMB.seq:

6: /cqn2_E/ptodata/1/ina/backfiles1.seq:
                                           GenCore version 4.5 Capyright (c) 1993 · 2000 Compugen Ltd.
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US-08-427-077-5

US-08-427-077-5

US-08-428-977-5

US-08-428-978-17-8

US-08-400-266-9

US-08-400-268-9

US-08-400-268-9

US-08-400-268-9

US-08-400-268-9

US-08-400-208-9

US-08-123-705-21

US-08-123-705-21

US-08-123-705-21

US-08-313-766-41
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 100
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Perfect score:
Sequence:
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COMPUTER READBLE FORM:
WEDTUM TYPE: Floppy disk
COMPUTER: IBM FC COMPALISK
SOFTWARE: PATENTIN NATA: 10, Version #1.30
CURRENT APPLICATION NATA: 12,097
FILING DATE: 21-APR-195
CLASSIFICATION NUMBER: 4C-94
RELETANTION NUMBER: 4C-94
TELECOMMUNICATION INFORMATION:
REFERENCE/COCKET NUMBER: 4C-94
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION
                     APPLICANT: Meagher, Richard B.
APPLICANT: Sommers, Anne O.
TITLE OF INVENTION: Hetal Resistance Sequences and
TITLE OF INVENTION: Hensgenic Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
NOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
GENERAL INFORMATION:
APPLICANT: Meaghe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4. Application US/08975365
Patent No. 6011007
GENERAL INFORMATION:
APPLICANT: Harbind, Svend
APPLICANT: Johnsen, John
APPLICANT: Andersen, John
APPLICANT: Andersen, John
APPLICANT: Andersen, John
APPLICANT: Andersen, John
APPLICANT: Activated 
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Length 100;
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STATE: New York
COUNTRY: United States of America
LIP: 1014-6401
COMPUTER READABLE FORM:
WEDIOW TYPE: FIDEPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
SOFTWAR: PR-COMPATIBLE
SOFTWARE: PR-COMPATIBLE
COMPATIAN APPLICATION DATA:
APPLICATION NUMBER: US/08/975,365
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0.5%; Score 26; DB 3; DB 3t Local Similarity 55.6%; Pred. No. 6.18+02; Matches 50; Conservative 0; Mismatches 40;
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR.1995
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Blias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELEPHONE: 212-667-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4529 tatttacataaagactgtgctgagaagcag 4558
                                                                                                                                       37 CAATTGGAAACTACTGTGCTTAGACGCAG 8
                                                                                                                                                                                                   TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-975-365-4/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Weagher, Richard B.
APPLICANT: Summers, Anne O.
APPLICANT: Summers and TITLE OF INVENTION: Transgenic Plants
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sulliven, P.C.
STREET: S370 Manhattan Circle, Suite 201
CITY: Boulder
                                                                                                                                                                                                                                      Qy 3086 ttgattttctacaagcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                         62 GTGAGCATACTCAAGCAAGCCAAGTTGCCTATAT 95
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; Sequence 5, Application US/08878957
; Patent No. 5965796
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Sequence 5, Application US/08427097 Patent No. 5658294

RESULT 3 US-08-427-097-5

us-09-676-436-3.szlm100.rni

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Ouery Match: 0.5%; Score 24.6; DB 1, Length 71; Best Local Similarity 65.5%; Pred. No. 1.2e+03; Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps
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Db 6 GAAGWCTAACAAGTAGTAAAAAA.ch.ncccccccrgacocartStcctc 2
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Sequence 78, Application US/08458424B
Sequence 78, Application US/08458424B
Sequence 78, Application US/08458424B
Sequence 78, Application US/08458424B
SEQUENCE TEMELOPE J. TOOTHANN
APPLICANT: TARNY GUIST
APPLICANT
APP
/ inear
// MOLECULE TYPE: DNA
US-08-458-423A-78
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0.54: Scorc 25.2; DB 2; Length 99:
Best Local Similarity 54.39; Preci No. 1u-03;
Matches 51: Condervative 0; Mismatches 43; Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ANGACCCACCATAGGGGAAGGTGTTACTGCATTGCGCATTGCATGGAAGGCATTGAAGTGC 61
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ZIP: 0011

CMPUTER READABLE FORM:
HEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OFFRATIMG SYSTEM: WS-DOS
SOFTMARE: Wordferfect 5.1
CURENT APPLICATION DATA:
APPLICATION NUMBER: 15,08/458,423A
FILLIGN DATE: 2-JUNE-1995
CLASSIFICATION: 55
             COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
CONFUTER: 1M PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREVENTIOR RELEASE #1.0, Version #1.30
CURRENT APPLICATION NOTE:
APPLICATION NUMBER: US/OB/878.957
FILING DATE: 19-TON: 800
PRIOR APPLICATION NOTE: 31-APPLICATION NUMBER: 31-APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
GS-486-4134-78/C
Sequence 78, Application US/08458423A
Sequence 78, Application US/08458423A
Setent No. 5731144
GAPLICANT: STEVEN RIGGOIST
APPLICANT: STEVEN RIGGOIST
APPLICANT: STEVEN RIGGOIST
APPLICANT: ALMEN GOLD
TITLE OF INVENTION: HIGH AFFINITY TGFN NUCLRIC
TITLE OF INVENTION: ACLO LIGANDS AND INHIBITORS
CORRESPONDENCES: 89
CORRESPONDENCE ADDRESS:
STATE: 6402 Eact Prentice Avenue, Sulte 4203
CITY: Deniver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3086 ttgattttctacaagcaattgaacctgcctttat 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GTGAGCATACTCAAGCAAGCCAAGTTGCCTATAT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLGST: lines:
MOLDOLLE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHRRACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
SYRANDEDNESS: aingle
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PRICING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/46,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/ARD INFORMATION:
NAME: BATTY J. SWANGON
REGISTRATION NUMBER: 33.215
REFRERENCEDCACET NUMBER:
TELEPHONE: (303) 793-3333
TELEPHONE: (303) 793-3333
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 DASE PAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458.423
FILING DATE: 02-3UNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Malch
Best Local Similarity 65.5'
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOLECULE TYPE: DNA US-08-973-124-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.5%; Score 24.6; DB 1; Length 71; Best Local Similarity 65.5%; Pred. No. 1.2e+03; Matches 36; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.5 inch, 1.44 Mb storage
COMPUTER: TBM COMPACIDLE
OPPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
CLASSIFICATION: 336
PRIOR PAPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996
PROR APPLICATION NUMBER: 08458,423
FILING DATE: 02-JUNE-1995
FRICH DATE: 03-JUNE-1995
FRICH DATE: 03-JUNE-1995
FRICH DATE: 03-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-1973-124-7B/C
US-08-1973-124-7B/C
Sequence 78 Application US/08973124
Patent No. 6207B16
GENERAL INFORMATION:
APPLICATI LARRY GOLD et al.
TITLE OF INVERTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVERTION: LIGANDS TO GROWTH
TITLE OF INVENTION: FACTORS
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Swanson & Bratschun, L.L.C. STRET: 8400 E. Prentice Avenue, Swite 200 SITE: Englewood STATE: Colorado
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:

APPLICATION DATA:
FILING DATE: 21-CTOBER-1992
PRIOR APPLICATION NUMBER: 07/964,624
FILING DATE: 3-CTOBER-1992
APPLICATION NUMBER: 08/11/991
FILING DATE: 8-SEPTEMBER-1993
APPLICATION NUMBER: 07/931,473
FILING DATE: 9-SEPTEMBER-1993
ATTORNEY/AGENT INFORMATION:
AMME: DAAR B. NCCLOBATO
REGISTRATION NUMBER: 33.960
REFERENCE/DOCKET NUMBER: NEX 34-7
TELECOMMULICATION INFORMATION:
TELEPHONE: (303) 793-333
INFORMATION FOR SEQ ID NO: 78:
SEDUENCE CHARACTERISTICS:
LEMCHF: 71 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
MOLECULE TYPE: DARA
                                                                                                                                                                                                                                                                                                                                                            NEX 34-2
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3958 gaacatgtgattaggctgtattcaaagcagatcaccattgcgatcaacgtcctcc 4012
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PCT-USSG-0014-78/C

Sequence 79 Application PC/TUS9608014

Sequence 79 Application PC/TUS9608014

Sequence 79 Application PC/TUS9608014

SEPENCE 70 APPLICATION TO THE PERIODE APPLICATION TO THE OF INVENTION TITLE OF INVENTION THE OF INVENTION TO THE OF THE OF INVENTION TO THE OF TH
0.5%; Score 24.6; DB 4; Length 71;
65.5%; Pred. No. 1.2e+03;
Live 0; Mismatches 19; Indels
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NEDIDIN TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM competible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Swangon & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
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APPLICANT Havelund, Swend
APPLICANT Havelund, Swend
APPLICANT Havelund, John
APPLICANT Andersen, Asser Sloth
APPLICANT Andersen, Asser Sloth
APPLICANT ANDERSEN, Asser Sloth
TIME OF INVENTION: ACTUATED INSULIN
WINNER OF SEQUENCES:
CORRESPONDENCE ADORESS:
ADDRESSEE: W. D. 57504970 No. 57504971h Americe. Inc.
STREET: 405 ICKNIGGEN ANDORES, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Macch U.54: Score 24.6; DB 3; Length 72: Beas Jobal Similarity 59.2%; Pract No. 1.38-03; Jacobs Macches 42; Conservative O: Mismatches 29; Indels O: Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 405 Icxington Avonuc, 64th Floor CITY: New York STATE: New York COUNTRY. United States of America 2.P.: 10174-640.
COMPUTER READABLE FORM: NEW YORK: READABLE FORM: NEW YORK: IBM PC COMPUTER: IBM PC CONTACTION OF SOFTHAIRS PATENT FOR SYSTEM: PC-055/MS-DOS SOFTHARE: PATENT IN RELEASE 11.0. Version $1.25 CURRENT APPLICATION DAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION BAIA:

FILING DATE: 03-MA-295
FILING DATE: 03-MA-295
CLASSTPCATION: 514
ATTORNY/ACET INFORMATION:
MACHE LAMBITIS. Elias J.
REGISTRATION WOMBER: 3965.226-US
FRIEDRAME: 212-86-023
TRIEPRAM: 212-86-023
TRIEPRAM: 212-86-023
TRIEPRAM: 212-86-023
TRIEPRAM: 100 DB 9:
SEQUENCE CHANACTERISTICS:
LENGTH: 100 DB 80 PAIA
TTER MACHEL CHANACTERISTICS:
TRANBERGES: CANACTERISTICS:
AMORECULE TYPE: CNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEXGUT. WERSELT. US. 08-400-256-9/c
US-08-400-256-9/c
Sequence 9. Application US/08400256
Fplant Mo. 5750439;
GRERAL INFORMATION:
             TELECOMUNICATION INFORMATION:
TELEFAKE: 201-487-58C
TELEFAK: 201-343-16C4
TELEKE: 133521
INFORMATION FOR SEQ IT NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STARNEDENESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-100-664A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-100-664A-5
Sequence 5, Application US/09100664A
Sequence 10, Application US/09100664A
Sequence 5, Application US/09100664A
SPECAT: TOWN.
SPECAT: TOWN.
SPECAT: TOWN.
SPECAT: BLAU, UNSTN
SPECAT: BLAU, UNSTN
SPECAT: BLAU, UNSTN
SPECAT: BLAU, UNSTN
SPECAT: SLAU, UNSTN
SEQUENCES: 13
SORRESSEE: ALAUDERSE: 13
STREET: 411 Machemack Avenue, 4th Floor
Unarkensack
STREET: 411 Machemack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER NEADABLE FORM:
NEDIOUM TIPE: Tloppy disk
NEDIOUM TIPE: Tloppy disk
COMPUTER: 18M PC compalible
OPERATIO STEER: PC-DOS/M9-DOS
COMPRETE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION MANBER: DS/G9/100.664A
FILING DATE: J9-JUN-1998
CLASSIPICATION H998
CLASSIPICATION H998
ATGHERS-JOACHEN INFORMATION:
NAME: JOACHEN INFORMATION:
NAME: JOACHEN INFORMATION:
REFERSENCE/POCKET WINDER: 26.74.7
REFERSENCE/POCKET WINDER: 26.74.7
PRIOR APPLICATION DATA:

APPLICATION MARER: 08/465,594
FILING DATE: 05-40NE-1995
PRIOR APPLICATION DATA: 1995
PRIOR APPLICATION DATA: 08/465,591
FILING DATE: 05-40NE-1995
FILING DATE: 07-40NE-1995
PRIOR APPLICATION DATA: 08/479,725
PRIOR APPLICATION DATA: 08/479,725
PRIOR APPLICATION DATA: 08/479,783
PRIOR APPLICATION DATA: 08/479,783
PRIOR APPLICATION DATA: 08/479,783
PRIOR APPLICATION DATA: 1995
APPLICATION NUMBER: 08/418
FILING DATE: 20-ANACH-1996
ATTORNAT/ACENT INFORMATION: NAME: BALLY SWANGON: 1805
REGISTATION INFORMATION: REGISTATION INFORMATION: TELEFONDUMICATION POR SEQ ID NO: 78: 126EPMS: 1333
TELEFAX: (133) 793-333
TELEFAX: (133) 793-333
TELEFAX: 71 DASE PALITS
LENGTH: 71 DASE PALITS
TYPE: DATA PALITS
TYPE: TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: 8ir;
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US96-08014-78
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CURTAIN 19898
COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . JOUNGY: Linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base palrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1180 agtgaagaagaa 1191
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LOCATION: 2..88
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
US-08-182-175A-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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US-08-975-365-9/C
US-08-975-365-9/C
Sequence 9, Application US/08975365
Sequence 9, Application
Sequence 10. 6011007
Sequence
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                                                                                                                                                                                                          Ouery Match 0.5%; Score 24.4; DB 1; Length 100; Best Local Similarity 54.4%; Pred. No. 1.7e+03; Matches 49; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTE: IBH PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE
TAPLICATION NUMBER: US/08/975,365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATE:
PRIOR APPLICATION DATE:
PRIOR APPLICATION NUMBER: US 08/400,256
FLING DATE: 03-MAR-1995
ATTORNEY/ACRY INFORMATION
NAME: LAMBLIA, Elias 3,728
REFERENCE/COCKET NUMBER: 33,728
REFERENCE/COCKET NUMBER: 33,728
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-867-0123
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
LEWGHT 100 DASE PAIRS
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4529 tatttacataaagactgtgctgagaagcag 4558
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4529 tatttacataaagactgtgctgagaagcag 4558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 CAATTGGAAACTACTGTGGTTAGACGCAG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10.74-64.01
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-D8-975-365-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GAAGATGAAGGCGATGGAGGAGAAGATGAAGTGGATGGAGATGAAGATGAAGTGGATGGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function= "synthetic storage protein /product= "protein" /gene= "ssp" /gene= "ssp" /standard_name= "5.11.11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.5%; Score 24: DB 1; Length 97; Best Local Similarity 58.3%; Pred. No. 2.2e+03; Matches 42; Conservative 0; Mismatches 30; Indels
CLASSIFICATION: 800
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATORNEY/AGENT INFORMATION:
AMME: LIND& Axamethy Floyd
REGISTRATION NUMBER: 33,692
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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us-09-676-436-3.szlml00.rni

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PRESULT 14
PET-1632-1612-54
Sequence 54, Application PC/TUS9206412
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Saverio Corl Faico
APPLICANT: Saverio Corl Faico
APPLICANT: Alact A Tace
APPLICANT: Allact A Tace
APPLICANT: Allact A Tace
APPLICANT: Allact A Tace
ADPRESSEE: E.I. du Pout de Nemours and Company
CORRESSORES:
ALACT A Tace
ALACT A Tace
APPLICANT: Allact A Tace
AP
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0.51: Score 24: 08 5: Tength 97:

deet Local Similarity 98:31: Pred. No. 2.2e+03:

Matchés 42: Conservative C: Mismatches 30: Indels 0: Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REMANLLE FORM:

LIP: 19898
COMPUTER REMANLLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER REMANLLE FORM:
COMPUTER: Macinicah
SOFTWARE: Macinicah
SOFTWARE: Macinicah
CURRENT APPLICATION
APPLICATION WINNER: EV/Jus27/06/12
FILING DATE: 19920807
FILING DATE: 9920807
FILING DATE: 9920807
FILING DATE: 9920807
FILING DATE: 9 ANGUSE 1991
ATTORREYAGRAT INCORMATION
NAME: Linda Axamethy £1094
RACISTRATION NUMBER: 33.692
REFERAN: (902) 992-4929
TELEFAX: (902) 992-4929
TELEFAX: (902) 992-4939
TELEFAX: (902) 902-4939
TELEFAX: (902) 902-4039
TELEFAX: (902) 902-40
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MOLECHIF TYPE: DNA (96007
ORIGINAL SOURCE: COLL
STRAIN: B. COLL
LMEDIATE SOURE:
DANEDIATE SOURE:
CLONE: 92-2
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
PCT-US92-06412-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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LOCATION: 2.88
OTHER INFORMATION: /function= synthetic
OTHER INFORMATION: storage protein
OTHER INFORMATION: Sproduce* protein
OTHER INFORMATION: /gene* sep*
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/product= 'protein'
/gene= 'ssp'
/ktandard.name=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
WEDDIN TYPE: ELOPET DISK
COMPUTER: IM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: MICROSOFT MORD VERSION 2.0C
CURRENT APPLICATION OATA:
APPLICATION NUMBER: US/08/474,533A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: E. T. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: MILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB-1037-C
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CAGASSIECRATION:

ACTORNEY/ACENT INFORMATION:

NAME: BARBARA C. SIECREL.

REGISTRATION NUMBER: 30.684

REFERENCE/CONCEY NUMBER: BB-10.

TELEPHONE: 302-992-491

TELEFAN: 302-79-0464

INFORMATION YOR SEQ IND W: 63:

SEQUENCE CHARACTERISTICS:

LEAGTH: 97 base pairs

TYPE: nuclec acid

STANDEDNESS: double
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CELL TYPE: DHS alpha
IMMEDIATE SOURCE:
CLONE: 92-2
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-474-6334-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DELAWARE COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: L
ORIGINAL SOURCE:
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Oy 1180 agtgaaqaagaa 1191

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70 AGAGAAGATCAA 81

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US-08-672-158A-8

1 Sequence 8, Application US/08672158A

1 Sequence 8, Application US/08672158A

1 Patent No. 577373

2 PALICANT: Sharyl Thompson

1 TILE OF INVENTION: Wolfication of Cryptic Splice Sites In

NUMBER OF SEQUENCES: 21

CORRESPONDERES: 22

CORRESPONDERES: 28

CORRESPONDERES: 30.

CORRESPO
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Search completed: May 29, 2002, 12:56:56 Job time: 9665 sec

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0; Gaps

Query Match

0.5%; Score 23.8; DB 1; Length 83;
Best Local Similarity 72.1%; Prod. No. 2.3e+03;
Matches 31; Conservative 0; Mismatches 12; Indels